

XX (GETH) GENENTECH INC.
 PA Adams S, Pan J, Zhong A;
 XX WPI; 2000-292842/25.
 XX N-PSDB; AAA14084.
 XX New nucleic acid encoding human uncoupled protein-4, useful e.g for
 PT identifying metabolic regulators for treatment of obesity.
 XX Claim 1; Fig 1; 80pp; English.
 XX This sequence represents human uncoupling protein UCP4. The human UCP4
 CC cDNA (ATCC 203124) was isolated from a brain cDNA library using a probe
 CC generated using primers AAA14086-AA14087. These primers were based on a
 CC UCP4 "from DNA" sequence (AAA14085) derived from a number of ESTs
 CC (expressed sequence tags) which were selected on the basis of homology
 CC with human UCP3. The human UCP4 gene has been mapped to chromosome 6p11.2
 CC -q12. UCP4 catalyzes the leakage of protons through the mitochondrial
 CC membrane, thus bypassing ATP synthase and thereby reducing the efficiency
 CC of ATP synthesis. Modulation of UCP4 activity or expression can therefore
 CC alter the metabolic rate and heat production via modulation of ATP
 CC synthetic efficiency. UCP4 nucleic acids may be used for recombinant
 CC production of UCP4 and as a source of primers and hybridisation probes
 CC which may be used for the analysis of UCP4 expression, for screening for
 CC homologous sequences, and for chromosome or gene mapping. They can be
 CC also be used to produce transgenic or knockout animals for the
 CC development and screening of therapeutic agents, as a source of antisense
 CC nucleotides, and in gene therapy for metabolic disorders. The UCP4
 CC protein can be used to screen for specific modulators of activity and to
 CC raise antibodies which may be used therapeutically as UCP4 antagonists or
 CC UCP4 targeting proteins, for affinity purification of UCP4, and as
 CC immunosay reagents for detecting UCP4 expression, e.g., for the
 CC diagnosis of impaired neural activity or neural degeneration. Agents that
 CC modulate UCP4 activity are used to control the metabolic rate in mammals.
 CC UCP4 upregulators can be used to increase the metabolic rate in order to
 CC treat obesity and the symptoms associated with stroke, trauma, sepsis and
 CC infection
 XX
 SQ Sequence 323 AA;
 Query Match 100.0%; Score 1690; DB 3; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2e-165;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSVPEEERLLPTQWRPRASKFLLSGCAATVAELATFPDLTKTRLQMGGAALRLGD 60
 DB 1 MSVPEEERLLPTQWRPRASKFLLSGCAATVAELATFPDLTKTRLQMGGAALRLGD 60
 QY 61 GARESAFYRCMVRTALGIIEEGFLKMQGVTALYRHVYVSGRMVYEHLEEVVFGKS 120
 DB 61 GARESAFYRCMVRTALGIIEEGFLKMQGVTALYRHVYVSGRMVYEHLEEVVFGKS 120
 QY 121 EDEHYPLKWSVIGMWAGVIGQFLNPTDLVKVQMGEGKRLKGLRPRGVHHAFAKI 180
 DB 121 EDEHYPLKWSVIGMWAGVIGQFLNPTDLVKVQMGEGKRLKGLRPRGVHHAFAKI 180
 QY 181 LAEGGIRGLWAGVPIQRAALVNMGLTFTYTKHYLVNLTPLEDNIMTHGLSSLCGSL 240
 DB 181 LAEGGIRGLWAGVPIQRAALVNMGLTFTYTKHYLVNLTPLEDNIMTHGLSSLCGSL 240
 QY 241 VASILGTPADVIKSRINQPRDKQGLLYKSTDCGLIQAVGEGFMSLYKGLFPLSWLRM 300
 DB 241 VASILGTPADVIKSRINQPRDKQGLLYKSTDCGLIQAVGEGFMSLYKGLFPLSWLRM 300
 QY 301 TPMSVMFWLTYEKIREMSGVSPF 323
 DB 301 TPMSVMFWLTYEKIREMSGVSPF 323
 ID XX
 AC XX
 XX AAY99457;
 DT 08-AUG-2000 (first entry)
 XX
 DE Human UCP4 amino acid sequence SEQ ID NO:406.
 XX
 KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
 KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
 XX
 OS Homo sapiens.
 XX
 PN WO200012708-A2.
 XX
 PD 09-MAR-2000.
 XX
 PF 01-SEP-1999; 99WO-US020111.
 XX
 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 PR 02-SEP-1998; 98US-0098843P.
 PR 09-SEP-1998; 98US-0098536P.
 PR 09-SEP-1998; 98US-0098596P.
 PR 09-SEP-1998; 98US-0098598P.
 PR 09-SEP-1998; 98US-0098602P.
 PR 09-SEP-1998; 98US-0098642P.
 PR 10-SEP-1998; 98US-0098741P.
 PR 10-SEP-1998; 98US-0098754P.
 PR 10-SEP-1998; 98US-0098763P.
 PR 10-SEP-1998; 98US-0098792P.
 PR 10-SEP-1998; 98US-0098808P.
 PR 10-SEP-1998; 98US-0098812P.
 PR 10-SEP-1998; 98US-0098815P.
 PR 10-SEP-1998; 98US-0098816P.
 PR 15-SEP-1998; 98US-0100385P.
 PR 15-SEP-1998; 98US-0100388P.
 PR 15-SEP-1998; 98US-0100390P.
 PR 16-SEP-1998; 98US-0100584P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100661P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100664P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100710P.
 PR 17-SEP-1998; 98US-0100711P.
 PR 17-SEP-1998; 98US-0100919P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100848P.
 PR 18-SEP-1998; 98US-0100849P.
 PR 18-SEP-1998; 98US-0101014P.
 PR 18-SEP-1998; 98US-0101068P.
 PR 18-SEP-1998; 98US-0101071P.
 PR 22-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0101471P.
 PR 23-SEP-1998; 98US-0101472P.
 PR 23-SEP-1998; 98US-0101474P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 23-SEP-1998; 98US-0101476P.
 PR 23-SEP-1998; 98US-0101477P.
 PR 23-SEP-1998; 98US-0101479P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101741P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101915P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 29-SEP-1998; 98US-0102207P.
 PR 29-SEP-1998; 98US-0102240P.
 PR 29-SEP-1998; 98US-0102307P.

PR	29-SEP-1998;	98US-0102330P.	DR	WPI; 2000-237871/20.
PR	29-SEP-1998;	98US-0102331P.	XX	N-PSDB; AAA37139.
PR	30-SEP-1998;	98US-0102484P.	XX	
PR	30-SEP-1998;	98US-0102487P.	PT	New mammalian DNA sequences encoding transmembrane, receptor or secreted
PR	30-SEP-1998;	98US-0102570P.	PT	PRO polypeptides, useful for screening of potential peptide or small
PR	30-SEP-1998;	98US-0102571P.	PT	molecule inhibitors of the relevant receptor/ligand interactions.
PR	01-OCT-1998;	98US-0102684P.	XX	
PR	01-OCT-1998;	98US-0102687P.	PS	Claim 12; Fig 236; 773pp; English.
PR	02-OCT-1998;	98US-0102965P.	XX	
PR	06-OCT-1998;	98US-0103258P.	CC	AAA37022 to AAA37144 encode the new isolated human transmembrane,
PR	07-OCT-1998;	98US-0103449P.	CC	receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
PR	07-OCT-1998;	98US-0103314P.	CC	transmembrane and receptor PRO proteins can be used for screening of
PR	07-OCT-1998;	98US-0103315P.	CC	potential peptide or small molecule inhibitors of the relevant
PR	07-OCT-1998;	98US-0103328P.	CC	receptor/ligand interactions. The polypeptides and nucleotide sequences
PR	07-OCT-1998;	98US-0103395P.	CC	encoding then have various industrial applications, including uses as
PR	07-OCT-1998;	98US-0103396P.	CC	pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
PR	07-OCT-1998;	98US-0103401P.	CC	primers and hybridisation probes used in the isolation of the PRO
PR	08-OCT-1998;	98US-0103633P.	CC	polypeptides from the present invention
PR	08-OCT-1998;	98US-0103678P.	XX	
PR	08-OCT-1998;	98US-0103679P.	SQ	Sequence 323 AA;
PR	08-OCT-1998;	98US-0103711P.		
PR	14-OCT-1998;	98US-0104257P.		
PR	20-OCT-1998;	98US-0104987P.		
PR	20-OCT-1998;	98US-0105000P.		
PR	20-OCT-1998;	98US-0105104P.		
PR	21-OCT-1998;	98US-0105169P.		
PR	22-OCT-1998;	98US-0105266P.		
PR	26-OCT-1998;	98US-0105933P.		
PR	26-OCT-1998;	98US-0105994P.		
PR	27-OCT-1998;	98US-0105807P.		
PR	27-OCT-1998;	98US-0105881P.		
PR	27-OCT-1998;	98US-0105882P.		
PR	27-OCT-1998;	98US-0106062P.		
PR	28-OCT-1998;	98US-0106023P.		
PR	28-OCT-1998;	98US-0106029P.		
PR	28-OCT-1998;	98US-0106030P.		
PR	28-OCT-1998;	98US-0106032P.		
PR	28-OCT-1998;	98US-0106033P.		
PR	28-OCT-1998;	98US-0106178P.		
PR	29-OCT-1998;	98US-0106248P.		
PR	29-OCT-1998;	98US-0106384P.		
PR	29-OCT-1998;	98US-0108500P.		
PR	30-OCT-1998;	98US-0106464P.		
PR	03-NOV-1998;	98US-0106856P.		
PR	03-NOV-1998;	98US-0106902P.		
PR	03-NOV-1998;	98US-0106905P.		
PR	03-NOV-1998;	98US-0106919P.		
PR	03-NOV-1998;	98US-0106932P.		
PR	03-NOV-1998;	98US-0106934P.		
PR	10-NOV-1998;	98US-0107783P.		
PR	17-NOV-1998;	98US-0108775P.		
PR	17-NOV-1998;	98US-0108779P.		
PR	17-NOV-1998;	98US-0108787P.		
PR	17-NOV-1998;	98US-0108788P.		
PR	17-NOV-1998;	98US-0108801P.		
PR	17-NOV-1998;	98US-0108802P.		
PR	17-NOV-1998;	98US-0108806P.		
PR	17-NOV-1998;	98US-0108807P.		
PR	17-NOV-1998;	98US-0108867P.		
PR	17-NOV-1998;	98US-0108925P.		
PR	18-NOV-1998;	98US-0108848P.		
PR	18-NOV-1998;	98US-0108849P.		
PR	18-NOV-1998;	98US-0108850P.		
PR	18-NOV-1998;	98US-0108851P.		
PR	18-NOV-1998;	98US-0108852P.		
PR	18-NOV-1998;	98US-0108858P.		
PR	18-NOV-1998;	98US-0108904P.		
XX		(GETH) GENENTECH INC.		
XX		Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;		
XX				
XX				

PR 01-SEP-1999; 99WO-US020111.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Deenoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX
 DR WPI; 2001-071395/08.
 XX
 PT Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy.
 XX
 PS Claim 1; Fig 236; 787pp; English.
 XX
 CC The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of anti-
 CC sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy
 XX
 SQ Sequence 323 AA;

Query Match 100.0%; Score 1690; DB 4; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2e-165;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSVPSEERLLPLTORWPRASKFLSGCAATVAELATFPDLTKTRLOMQGEAALRLGD 60
 DB 1 MSVPSEERLLPLTORWPRASKFLSGCAATVAELATFPDLTKTRLOMQGEAALRLGD 60
 QY 61 GARESAPYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYEHLEVVFGKS 120
 DB 61 GARESAPYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYEHLEVVFGKS 120
 QY 121 EDEHYPLWKSIVGGWAGVIGQFLANPTDLVKVQMQMEGKRKLEGPRLRFRGVHHAFAKI 180
 DB 121 EDEHYPLWKSIVGGWAGVIGQFLANPTDLVKVQMQMEGKRKLEGPRLRFRGVHHAFAKI 180
 QY 181 LAEGGIRGLWAGWPNVQRAALVNMGDLTYYDVTKHYLVLTNPLEDNIMTHGLSSLCSDL 240
 DB 181 LAEGGIRGLWAGWPNVQRAALVNMGDLTYYDVTKHYLVLTNPLEDNIMTHGLSSLCSDL 240
 QY 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIQAVQGEFGMSLYKGLFPSWLRM 300
 DB 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIQAVQGEFGMSLYKGLFPSWLRM 300
 QY 301 TPWSMVFWLTVEKIREMSGVSPF 323
 DB 301 TPWSMVFWLTVEKIREMSGVSPF 323

RESULT 4
 ID AAB87588 standard; protein; 323 AA.
 XX
 AC AAB87588;
 XX
 XX
 DT 15-MAY-2001 (first entry)
 XX
 DE Human PRO1566.
 XX
 KW Human; PRO protein; mapping.

XX Homo sapiens.
 OS WO200116318-A2.
 XX
 PN 08-MAR-2001.
 PD
 XX
 PF 24-AUG-2000; 2000WO-US023328.
 XX
 XX 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 07-DEC-1999; 99US-0169495P.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-JAN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 25-APR-2000; 2000US-0199397P.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 05-JUN-2000; 2000US-0209832P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
 PI
 XX
 DR WPI; 2001-183260/18.
 DR N-PSDB; AAF92120.
 XX
 PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
 PT biology, including use as hybridization probes, and in chromosome and
 PT gene mapping.
 XX
 PS Claim 12; Fig 126; 278pp; English.
 XX
 CC The present sequence is a human PRO polypeptide (secreted and
 CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
 CC anti-PRO antibodies are useful for preparation of a medicament useful in
 CC the treatment of a condition which is responsive to the PRO protein.
 CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
 CC employed as molecular weight markers for protein electrophoresis. The PRO
 CC coding sequence has applications in molecular biology, including use as
 CC hybridisation probes, and in chromosome and gene mapping
 XX
 SQ Sequence 323 AA;
 Query Match 100.0%; Score 1690; DB 4; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2e-165;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSVPSEERLLPLTORWPRASKFLSGCAATVAELATFPDLTKTRLOMQGEAALRLGD 60
 DB 1 MSVPSEERLLPLTORWPRASKFLSGCAATVAELATFPDLTKTRLOMQGEAALRLGD 60
 QY 61 GARESAPYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYEHLEVVFGKS 120
 DB 61 GARESAPYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYEHLEVVFGKS 120
 QY 121 EDEHYPLWKSIVGGWAGVIGQFLANPTDLVKVQMQMEGKRKLEGPRLRFRGVHHAFAKI 180
 DB 121 EDEHYPLWKSIVGGWAGVIGQFLANPTDLVKVQMQMEGKRKLEGPRLRFRGVHHAFAKI 180
 QY 181 LAEGGIRGLWAGWPNVQRAALVNMGDLTYYDVTKHYLVLTNPLEDNIMTHGLSSLCSDL 240
 DB 181 LAEGGIRGLWAGWPNVQRAALVNMGDLTYYDVTKHYLVLTNPLEDNIMTHGLSSLCSDL 240
 QY 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIQAVQGEFGMSLYKGLFPSWLRM 300
 DB 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIQAVQGEFGMSLYKGLFPSWLRM 300

QY 301 TPWSMVFWLTYEKIRMSGVSPF 323
 |||||
 Db 301 TPWSMVFWLTYEKIRMSGVSPF 323

RESULT 5
 ABG95913
 ID ABG95913 standard; protein; 323 AA.
 AC ABG95913;
 XX
 DT 10-DEC-2002 (first entry)
 XX
 DE Human secreted/transmembrane protein PRO1566.
 XX
 KW Human; secreted protein; transmembrane protein; antirheumatic;
 KW antiarthritic; osteopathic; sports-related joint problem;
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US2002119130-A1.
 XX
 PD 29-AUG-2002.
 XX
 PF 06-DEC-2001; 2001US-00006867.
 XX
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 22-APR-1998; 98US-0082797P.
 PR 29-APR-1998; 98US-0083495P.
 PR 15-MAY-1998; 98US-0085579P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088030P.
 PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088740P.
 PR 10-JUN-1998; 98US-0088811P.
 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088825P.
 PR 11-JUN-1998; 98US-0088863P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 19-JUN-1998; 98US-0089952P.
 PR 22-JUN-1998; 98US-0090246P.
 PR 24-JUN-1998; 98US-0090444P.
 PR 25-JUN-1998; 98US-0090688P.
 PR 25-JUN-1998; 98US-0090696P.
 PR 26-JUN-1998; 98US-0090862P.
 PR 02-JUL-1998; 98US-0091828P.
 PR 10-AUG-1998; 98US-0096012P.
 PR 17-AUG-1998; 98US-0096757P.
 PR 18-AUG-1998; 98US-0096949P.
 PR 18-AUG-1998; 98US-0096959P.
 PR 26-AUG-1998; 98US-0097954P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 26-AUG-1998; 98US-0097979P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099815P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100663P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 22-SEP-1998; 98US-0101279P.

PR 23-SEP-1998; 98US-0101475P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 24-SEP-1998; 98US-0103570P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021194.
 PR 22-DEC-1999; 99WO-US030720.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 02-MAY-2000; 2000WO-US014042.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032378.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX
 DR WPI; 2002-731348/79.
 DR N-PSDB; ABS74440.
 XX
 XX New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating sports-related
 PT joint problems, osteoarthritis or rheumatoid arthritis.
 XX
 PS Claim 20; Fig 126; 399pp; English.
 XX
 CC The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing as
 CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
 CC extracellular domain of the proteins with their associated signal peptide
 CC or lacking its associated signal peptide. Also included are the nucleic
 CC acids encoding the proteins, vectors, host cells, fusion proteins and
 CC antibodies which specifically bind to the proteins. The proteins are
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample
 CC suspected of containing an A, B, C or D polypeptide, by contacting the
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
 CC conjugate in the sample, where the formation of the conjugate is
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 CC H or I polypeptide is labeled with a detectable label or is attached to a
 CC solid support. The proteins are useful for linking a bioactive molecule
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 CC or I, or antibodies against them are useful for modulating a biological
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for

identifying agonists or antagonists, for the preparation of a medicament useful in the treatment of a condition which is responsive to the proteins, as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. Nucleic acids encoding the proteins are useful as hybridisation probes, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, for the preparation of the proteins, to generate transgenic or knockout animals which are useful in the development and screening of therapeutic useful reagents, for chromosome identification, and in gene therapy. The antibody is useful as a therapeutic agent, in a diagnostic assay and for affinity purification of the protein from recombinant cell culture natural sources. The present sequence represents a novel secreted or transmembrane protein of the invention

Query Match 100.0%; Score 1690; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 2e-165;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSVPEEERLLPLTQWRPRASKFLLSGCAATVAELATFPDLTKTRLQMGGAALRLGD 60
DB 1 MSVPEEERLLPLTQWRPRASKFLLSGCAATVAELATFPDLTKTRLQMGGAALRLGD 60
QY 61 GAREAPYRGWVRTALGIIIEEGFLKMQGVTPAIYRHVYVSGRMVYEHLEVVFGKS 120
DB 61 GAREAPYRGWVRTALGIIIEEGFLKMQGVTPAIYRHVYVSGRMVYEHLEVVFGKS 120
QY 121 EDEHYPLWKSIVGGWAGVIGQFLANPTDLVKVQMGEGKRLKLEKPLRFRGVHAFAKI 180
DB 121 EDEHYPLWKSIVGGWAGVIGQFLANPTDLVKVQMGEGKRLKLEKPLRFRGVHAFAKI 180
QY 181 LAEGGIRGLWAGWPNVQRAALVNMGDLTTYDTVKHYLVNTPLEDNIMTHGLSSLCSGL 240
DB 181 LAEGGIRGLWAGWPNVQRAALVNMGDLTTYDTVKHYLVNTPLEDNIMTHGLSSLCSGL 240
QY 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIOAVQEGFMSLYKGFPLPSWLRM 300
DB 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIOAVQEGFMSLYKGFPLPSWLRM 300
QY 301 TPWSMVFWLTYEKIREMSGVSPF 323
DB 301 TPWSMVFWLTYEKIREMSGVSPF 323

RESULT 6
ABU90938
ID ABU90938 standard; protein; 323 AA.

AC ABU90938;
XX 11-JUL-2003 (first entry)
XX Novel human secreted and transmembrane protein PRO1566.
DE Human; secreted and transmembrane protein; PRO; antibody therapy;
XX pharmaceutical; diagnostic; biosensor; bioreactor.
XX Homo sapiens.
XX US2003018173-A1.
XX 23-JAN-2003.
XX 01-MAY-2002; 2002US-00063515.
XX 06-DEC-2001; 2001US-00006867.
XX (GETH) GENENTECH INC.
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2003-401702/38.
DR N-PSDB; ACA91226.
XX New antibody useful for identifying PRO polypeptides, for affinity purification of PRO polypeptides, and for preparing a medicament for diagnosing or treating conditions responsive to the antibody or PRO polypeptide.
XX Disclosure; Fig 126; 345pp; English.
XX The invention describes an antibody that specifically binds to a PRO polypeptide having a fully defined amino acid sequence given in the specification. The antibody is useful in identifying PRO polypeptides useful for various industrial applications, including pharmaceuticals, diagnostics, biosensors and bioreactors. The antibody is also used for affinity purification of PRO polypeptides from recombinant cell culture or natural sources. The antibody, PRO polypeptide, or its agonists or antagonists, may be used for preparing a medicament for diagnosing or treating a condition responsive to the antibody, PRO polypeptide, or its agonists or antagonists. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
XX Sequence 323 AA;

Query Match 100.0%; Score 1690; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 2e-165;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSVPEEERLLPLTQWRPRASKFLLSGCAATVAELATFPDLTKTRLQMGGAALRLGD 60
DB 1 MSVPEEERLLPLTQWRPRASKFLLSGCAATVAELATFPDLTKTRLQMGGAALRLGD 60
QY 61 GAREAPYRGWVRTALGIIIEEGFLKMQGVTPAIYRHVYVSGRMVYEHLEVVFGKS 120
DB 61 GAREAPYRGWVRTALGIIIEEGFLKMQGVTPAIYRHVYVSGRMVYEHLEVVFGKS 120
QY 121 EDEHYPLWKSIVGGWAGVIGQFLANPTDLVKVQMGEGKRLKLEKPLRFRGVHAFAKI 180
DB 121 EDEHYPLWKSIVGGWAGVIGQFLANPTDLVKVQMGEGKRLKLEKPLRFRGVHAFAKI 180
QY 181 LAEGGIRGLWAGWPNVQRAALVNMGDLTTYDTVKHYLVNTPLEDNIMTHGLSSLCSGL 240
DB 181 LAEGGIRGLWAGWPNVQRAALVNMGDLTTYDTVKHYLVNTPLEDNIMTHGLSSLCSGL 240
QY 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIOAVQEGFMSLYKGFPLPSWLRM 300
DB 241 VASILGTPADVIKSRIMNQPRDKQGRGLLYKSSDCLIOAVQEGFMSLYKGFPLPSWLRM 300
QY 301 TPWSMVFWLTYEKIREMSGVSPF 323
DB 301 TPWSMVFWLTYEKIREMSGVSPF 323

RESULT 7
ABO33997
ID ABO33997 standard; protein; 323 AA.
XX ABO33997;
XX 18-SEP-2003 (first entry)
XX Human secreted/transmembrane protein PRO1566.
XX Human; secreted/transmembrane protein; PRO; tumour; cancer; cytostatic.
XX Homo sapiens.
XX US2003009013-A1.
XX 09-JAN-2003.
XX

Db 61 GARESAPYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVYVSGRMVYEHLEWVFGKS 120
Qy 121 EDEHYPLWKSIVIGMMAGVIGQFLANPTDLVKVQMQMEGRKLEGGKPLRFRGVHAFPAKI 180
Db 121 EDEHYPLWKSIVIGMMAGVIGQFLANPTDLVKVQMQMEGRKLEGGKPLRFRGVHAFPAKI 180
Qy 181 LAEGGIRGLWAGWVNPVNIQRAALVNMGDLTYYDTVKHYLVLTNPLEDNIMTHGLSSLCGSL 240
Db 181 LAEGGIRGLWAGWVNPVNIQRAALVNMGDLTYYDTVKHYLVLTNPLEDNIMTHGLSSLCGSL 240
Qy 241 VASILGTPADVTKSRIMNPRDKQGRGLLYKSSDCLIQAVQGEFMSLYKGFPLPSWLRM 300
Db 241 VASILGTPADVTKSRIMNPRDKQGRGLLYKSSDCLIQAVQGEFMSLYKGFPLPSWLRM 300
Qy 301 TPWSMVFWLTYEKIREMSGVSPF 323
Db 301 TPWSMVFWLTYEKIREMSGVSPF 323

RESULT 10
ABU72349
ID ABU72349 standard; protein; 323 AA.
XX AC ABU72349;
XX DT 16-JUN-2003 (first entry)
XX DE Human PRO polypeptide #63.
XX KW Human; PRO polypeptide; secreted and transmembrane protein;
XX KW anti-PRO antibody; diagnostic assay; gene expression.
XX OS Homo sapiens.
XX PN US2002182638-A1.
XX PD 05-DEC-2002.
XX PF 02-MAY-2002; 2002US-00063547.
XX PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 25-AUG-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 28-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 23-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854208.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.

PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
PA (GETH) GENENTECH INC.
XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2003-328612/04.
DR N-PSDB; ACA64048.
XX An isolated secreted transmembrane polypeptide designated PRO, useful as
PT a therapeutic agent.
XX Disclosure; Fig 126; 236pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of a condition responsive to anti-PRO antibody.
CC Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting
CC its expression in specific cells, tissues or serum, and for affinity
CC purification of PRO from recombinant cell culture or natural sources.
CC ABU72287-ABU72370 represent the human PRO polypeptides of the invention
XX
XX Sequence 323 AA;
Qy 1 MSVPEEEERLLPLTORWPRASKFLLSGCAATVAELATFPDLTKRLQMGEEAALRLGD 60
Db 1 MSVPEEEERLLPLTORWPRASKFLLSGCAATVAELATFPDLTKRLQMGEEAALRLGD 60
Qy 61 GARESAPYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVYVSGRMVYEHLEWVFGKS 120
Db 61 GARESAPYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVYVSGRMVYEHLEWVFGKS 120
Qy 121 EDEHYPLWKSIVIGMMAGVIGQFLANPTDLVKVQMQMEGRKLEGGKPLRFRGVHAFPAKI 180
Db 121 EDEHYPLWKSIVIGMMAGVIGQFLANPTDLVKVQMQMEGRKLEGGKPLRFRGVHAFPAKI 180
Qy 181 LAEGGIRGLWAGWVNPVNIQRAALVNMGDLTYYDTVKHYLVLTNPLEDNIMTHGLSSLCGSL 240
Db 181 LAEGGIRGLWAGWVNPVNIQRAALVNMGDLTYYDTVKHYLVLTNPLEDNIMTHGLSSLCGSL 240
Qy 241 VASILGTPADVTKSRIMNPRDKQGRGLLYKSSDCLIQAVQGEFMSLYKGFPLPSWLRM 300
Db 241 VASILGTPADVTKSRIMNPRDKQGRGLLYKSSDCLIQAVQGEFMSLYKGFPLPSWLRM 300
Qy 301 TPWSMVFWLTYEKIREMSGVSPF 323
Db 301 TPWSMVFWLTYEKIREMSGVSPF 323

RESULT 11
ABU91022
ID ABU91022 standard; protein; 323 AA.
XX AC ABU91022;
XX DT 14-JUL-2003 (first entry)
XX DE Human PRO polypeptide #63.
XX KW Human; PRO polypeptide; secreted protein; transmembrane protein; rectal;
KW lung; stomach; oesophageal; skin; tumour; cancer; cytostatic.
XX OS Homo sapiens.

XX	US2003018168-A1.	Query Match	100.0%;	Score 1690;	DB 6;	Length 323;
PN		Best Local Similarity	100.0%;	Pred. No. 2e-165;		
XX		Matches 323;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
PD	23-JAN-2003.					
PF	02-MAY-2002;	1	MSVPEERLLPLTORWPRASKFLLSGCAATVAELATFPDLTKTRLQMOGAALRLGD	60		
XX		XX				
XX	30-DEC-1998;	1	MSVPEERLLPLTORWPRASKFLLSGCAATVAELATFPDLTKTRLQMOGAALRLGD	60		
PR	08-MAR-1999;	61	GARSAFYRGVMTALGIIIEEGFLKMOGVTPALYRHVVYSGRMVTVYHLEVVVFGKS	120		
PR	14-MAY-1999;	61	GARSAFYRGVMTALGIIIEEGFLKMOGVTPALYRHVVYSGRMVTVYHLEVVVFGKS	120		
PR	25-AUG-1999;	121	EDEHYPLWKSVIGGMWAGVIGQFLANPTDLVKVQMQMEGRKLEKPLFRGVHFAFI	180		
PR	25-AUG-1999;	121	EDEHYPLWKSVIGGMWAGVIGQFLANPTDLVKVQMQMEGRKLEKPLFRGVHFAFI	180		
PR	25-AUG-1999;	181	LAEGGIRGLWAGVNPVQRAALVNMGDLTYYTVKHVLTNPLEDNIMTHGLSSLCSSL	240		
PR	15-SEP-1999;	181	LAEGGIRGLWAGVNPVQRAALVNMGDLTYYTVKHVLTNPLEDNIMTHGLSSLCSSL	240		
PR	18-OCT-1999;	241	VASILGTPADVIKSRIMNQPRDKQGRGLLYKSTDCLIQAVQEGFMSLYKGFPLPSWLRM	300		
PR	12-NOV-1999;	241	VASILGTPADVIKSRIMNQPRDKQGRGLLYKSTDCLIQAVQEGFMSLYKGFPLPSWLRM	300		
PR	30-DEC-1999;	301	TPWSMVFWLTIEKIREMSGVSPF	323		
PR	18-FEB-2000;	301	TPWSMVFWLTIEKIREMSGVSPF	323		
PR	01-MAR-2000;					
PR	02-MAR-2000;					
PR	21-MAR-2000;					
PR	22-MAY-2000;					
PR	02-JUN-2000;					
PR	22-AUG-2000;					
PR	18-SEP-2000;					
PR	08-NOV-2000;					
PR	10-NOV-2000;					
PR	01-DEC-2000;					
PR	20-DEC-2000;					
PR	28-FEB-2001;					
PR	22-MAR-2001;					
PR	10-MAY-2001;					
PR	30-MAY-2001;					
PR	01-JUN-2001;					
PR	05-JUN-2001;					
PR	29-JUN-2001;					
PR	18-JUL-2001;					
PR	06-DEC-2001;					
XX	(GETH) GENENTECH INC.					
XX	Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;					
PI	Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;					
PI	WPI; 2003-401699/38.					
XX	N-PSDB; ACA91312.					
DR						
XX	New isolated, secreted and transmembrane PRO polypeptide, useful for the					
PT	diagnosis, prevention and treatment of rectal, lung, stomach, esophageal					
PT	or skin cancers.					
XX	Disclosure; Fig 126; 235pp; English.					
PS						
XX	The present invention relates to the isolation of novel human PRO					
CC	polypeptides, and the polynucleotide sequences encoding them. The PRO					
CC	polypeptides are secreted and transmembrane proteins. The PRO polypeptide					
CC	and polynucleotide sequences are useful for the diagnosis, prevention and					
CC	treatment of rectal, lung, stomach, oesophageal or skin tumours, and/or					
CC	cancers. The PRO polypeptides are also useful as molecular weight					
CC	markers. The PRO polynucleotide sequences are useful for chromosome					
CC	identification, hybridisation probes, and for screening libraries of					
CC	human cDNA, genomic DNA or mRNA. They may also be used in gene therapy,					
CC	particularly for replacing a defective gene. ABU90960-ABU91043 represent					
XX	the human PRO polypeptides of the invention					
XX	Sequence 323 AA;					
SQ						

PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 30-MAY-2001; 2001US-00854280.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 29-JUN-2001; 2001US-00869599.
 PR 18-JUL-2001; 2001US-00908827.
 PR 08-DEC-2001; 2001US-00006867.
 XX (GETH) GENENTECH INC.
 PA Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX WPI; 2003-447383/42.
 DR N-PSDB; ACD45211.
 XX
 PT New isolated antibody specifically binding a PRO polypeptide, useful for
 PT the preparation of a medicament for treating disorders with the aberrant
 PT expression or activity of the PRO polypeptide, such as tumor conditions
 PT and cancer.
 XX
 XX Disclosure; Fig 126; 223pp; English.
 XX
 CC The invention relates to an antibody that binds to a secreted and
 CC transmembrane PRO polypeptide. The methods and compositions of the
 CC present invention are useful for the preparation of a medicament for the
 CC treatment of disorders associated with the aberrant expression or
 CC activity of the PRO polypeptide, such as tumor conditions and cancer.
 CC They can also be used to generate transgenic or knockout animals useful
 CC in the development and screening of therapeutically useful reagents. The
 CC PRO polypeptides and encoding nucleic acids can be used as molecular
 CC weight markers for protein electrophoresis, chromosome identification and
 CC tissue typing. The antibodies may be used in various diagnostic and
 CC competitive binding and/or immunoprecipitation assays. The present
 CC sequence represents the amino acid sequence of a secreted and
 CC transmembrane PRO polypeptide
 XX
 SQ Sequence 323 AA;
 Query Match 100.0%; Score 1690; DB 6; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2e-165;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSVPEEEERLLPTQWRPRASKFLLSGCAATVAELATFFLDLTQRLQMGEEAALRLGD 60
 DB 1 MSVPEEEERLLPTQWRPRASKFLLSGCAATVAELATFFLDLTQRLQMGEEAALRLGD 60
 QY 61 GAREAPYRGWRTALGIIIEEGFLKMQGVTPAIYRHVVYSGRMVYVYHLEVVFGKS 120
 DB 61 GAREAPYRGWRTALGIIIEEGFLKMQGVTPAIYRHVVYSGRMVYVYHLEVVFGKS 120
 QY 121 EDEHYPLWKSIVGGMAGVIGQFLANPTDLVKVQMQEGKRLGKPLRFRGVHFAFAKI 180
 DB 121 EDEHYPLWKSIVGGMAGVIGQFLANPTDLVKVQMQEGKRLGKPLRFRGVHFAFAKI 180
 QY 181 LAEGGIRGLWAGVNPVQRAALVNMGLTYYDVTGVHLVNTPLEDNIMTHGLSSLCISGL 240
 DB 181 LAEGGIRGLWAGVNPVQRAALVNMGLTYYDVTGVHLVNTPLEDNIMTHGLSSLCISGL 240
 QY 241 VASILGTADVIKSRIMNQPRDQKRGLLYSKSTDCLIQAVQEGFMSLYKGLFPLSWLRM 300
 DB 241 VASILGTADVIKSRIMNQPRDQKRGLLYSKSTDCLIQAVQEGFMSLYKGLFPLSWLRM 300
 QY 301 TPWSMVFWLTYEKIREMSGVSPF 323
 DB 301 TPWSMVFWLTYEKIREMSGVSPF 323

RESULT 13
 ABU92538
 ID ABU92538 standard; protein; 323 AA.
 XX AC ABU92538;
 XX DT 17-JUL-2003 (first entry)
 DE Human secreted/transmembrane protein PRO1566.
 XX Human; PRO; secreted protein; transmembrane protein; cytostatic;
 KW vulvar; osteopathic; antiarthritic; antirheumatic; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tumour necrosis factor; pericyte cell proliferation;
 KW TNF-alpha; proteoglycans release; cartilage; cancer; wound healing;
 KW cartilage defect; osteoarthritis; rheumatoid arthritis.
 XX OS Homo sapiens.
 XX US2003045684-A1.
 XX PD 06-MAR-2003.
 XX PF 02-MAY-2002; 2002US-00063553.
 XX PR 30-DEC-1998; 98KR-00062142.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380142.
 PR 15-SEP-1999; 99US-00397342.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 30-DEC-1999; 99WO-US031274.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 02-JUN-2000; 2000WO-US014042.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 28-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 30-MAY-2001; 2001US-00854280.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 29-JUN-2001; 2001US-00869599.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-DEC-2001; 2001US-00006867.
 XX (GETH) GENENTECH INC.
 PA Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX WPI; 2003-392892/37.
 DR N-PSDB; ACA93759.
 XX New PRO994 polypeptide, useful for detecting tumors, or for stimulating

PT Tumor Necrosis Factor alpha, or pericyte proliferation, especially for
PT treating cancer, cartilage defects, osteoarthritis and rheumatoid
PT arthritis in a mammal.
XX Disclosure; Fig 126; 235pp; English.
XX
PS The invention relates to a new isolated PRO994 polypeptide comprises an
CC amino acid sequence appearing as ABU92499, PRO994 lacking its associated
CC signal peptide, the extracellular domain of PRO994, the extracellular
CC domain of PRO994 (lacking its associated signal peptide) or the protein
CC encoded by the full-length coding sequence of the cDNA ATCC 203018. Also
CC included is a chimeric molecule comprising the PRO994 polypeptide fused
CC to a heterologous amino acid sequence. The PRO polypeptide is useful in
CC pharmaceuticals, diagnostics, biosensors or bioreactors. It is
CC particularly useful for detecting tumours (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of tumour necrosis factor (TNF)-
CC alpha from human blood, for stimulating the proliferation of pericyte
CC cells, or stimulating the release of proteoglycans from cartilage. The
CC polypeptide may be employed for a variety of therapeutic purposes, e.g.
CC for treating cancer, wound healing, cartilage defects, osteoarthritis,
CC rheumatoid arthritis. Also disclosed are the cDNA encoding PRO994, 83
CC other PRO polypeptides and their encoding cDNAs. The present sequence
CC represents a PRO polypeptide of the invention
XX
XX Sequence 323 AA;

Query Match 100.0%; Score 1690; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 2e-165;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSVPEERLLPTQWPRASKFLLSGCAATVAELATFPLDLTKRLQMOGEAALRLGD 60
Db 1 MSVPEERLLPTQWPRASKFLLSGCAATVAELATFPLDLTKRLQMOGEAALRLGD 60
Qy 61 GAREAPYRGVMTALGIIEEGFLKMQGVTPTAIYRHVYVSGRMVYEHLEVVFGKS 120
Db 61 GAREAPYRGVMTALGIIEEGFLKMQGVTPTAIYRHVYVSGRMVYEHLEVVFGKS 120
Qy 121 EDEHYPLWKSIVGGMAGVIGQFLANPTDLVKVQMOEGKRLGKPLRFRGVHFAFI 180
Db 121 EDEHYPLWKSIVGGMAGVIGQFLANPTDLVKVQMOEGKRLGKPLRFRGVHFAFI 180
Qy 181 LAEGIRGLWAGVNPQRAALVNMGLTYYTVGHVYLVNTPLEDNIMTHGLSSLCISGL 240
Db 181 LAEGIRGLWAGVNPQRAALVNMGLTYYTVGHVYLVNTPLEDNIMTHGLSSLCISGL 240
Qy 241 VASILGTPADVKSIRINQPRDKQGRGLLYKSSDCLIQAVQGEFMSLYKGLPSWLRM 300
Db 241 VASILGTPADVKSIRINQPRDKQGRGLLYKSSDCLIQAVQGEFMSLYKGLPSWLRM 300
Qy 301 TPWSMVFWLTYEKIREMSGVSPF 323
Db 301 TPWSMVFWLTYEKIREMSGVSPF 323

RESULT 14
ABU81208
ID ABU81208 standard; protein; 323 AA.
XX
AC ABU81208;
XX
XX 23-JUN-2003 (first entry)
XX Human secreted polypeptide PRO1566.
XX Human; affinity purification.
XX Homo sapiens.
OS US2003027212-1A1.
PN 06-FEB-2003.
PD

XX 02-MAY-2002; 2002US-00063544.
PF 30-DEC-1998; 98KR-00062142.
XX 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US0031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00742599.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
XX (GETH) GENENTECH INC.
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2003-341840/32.
DR N-PSDB; ACA67333.
XX
XX New monoclonal antibody that binds to a secreted and transmembrane
PT polypeptide, useful for detecting and purifying the polypeptide and also
PT for treating conditions responsive to the antibody.
XX
XX Disclosure; Fig 126; 235pp; English.
XX
XX The invention relates to an antibody that binds to a secreted and
CC transmembrane polypeptide, PRO1136. The antibody is useful for preparing
CC a medicament useful in the treatment of a condition responsive to anti-
CC PRO antibody. The antibody is also useful in diagnostic assays for PRO,
CC by detecting its expression in specific cells, tissues or serum, and for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. The present sequence represents a cDNA encoding a PRO
CC polypeptide of the invention
XX
XX Sequence 323 AA;

Query Match 100.0%; Score 1690; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 2e-165;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSVPEERLLPTQWPRASKFLLSGCAATVAELATFPLDLTKRLQMOGEAALRLGD 60
Db 1 MSVPEERLLPTQWPRASKFLLSGCAATVAELATFPLDLTKRLQMOGEAALRLGD 60

Qy	61	GARESAFYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYEHLEWVFGKS	120
Db	61	GARESAFYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYEHLEWVFGKS	120
Qy	121	EDEHYPLWKSIVIGMMAGVIGQFLANPTDLVKVQOMEGKRLKLGKPLRPRGVHHAFAKI	180
Db	121	EDEHYPLWKSIVIGMMAGVIGQFLANPTDLVKVQOMEGKRLKLGKPLRPRGVHHAFAKI	180
Qy	181	LAEGGIRGLWAGWVPNIQRAALVNMGDLTYYDTVKHYLVNLTPLEDNIMTHGLSSLCSGL	240
Db	181	LAEGGIRGLWAGWVPNIQRAALVNMGDLTYYDTVKHYLVNLTPLEDNIMTHGLSSLCSGL	240
Qy	241	VASILGTPADVIKSRIMNQPRDKQGRGLLYKSTDCCLIQAVQEGFMSLYKGLPWSLWRM	300
Db	241	VASILGTPADVIKSRIMNQPRDKQGRGLLYKSTDCCLIQAVQEGFMSLYKGLPWSLWRM	300
Qy	301	TPWSMVFWLTYEKIREMSGVSPF 323	
Db	301	TPWSMVFWLTYEKIREMSGVSPF 323	
RESULT 15			
ID	ABO53322		
XX	AC	ABO53322 standard; protein; 323 AA.	
XX	AC	ABO53322;	
DT	14-OCT-2003	(first entry)	
XX	XX	Novel human secreted and transmembrane protein PRO1566.	
DE	XX	Human; secreted and transmembrane protein; PRO.	
KW	XX	Homo sapiens.	
OS	XX	US2003027986-A1.	
PN	XX	06-FEB-2003.	
PD	XX	02-MAY-2002; 2002US-00063549.	
PF	XX	30-DEC-1998; 98KR-00062142.	
PR	PR	08-MAR-1999; 99WO-US005028.	
PR	PR	14-MAY-1999; 99US-00311832.	
PR	PR	14-MAY-1999; 99WO-US010733.	
PR	PR	25-AUG-1999; 99US-00380137.	
PR	PR	25-AUG-1999; 99US-00380138.	
PR	PR	25-AUG-1999; 99US-00380139.	
PR	PR	15-SEP-1999; 99US-00397342.	
PR	PR	18-OCT-1999; 99US-00403297.	
PR	PR	12-NOV-1999; 99US-00423844.	
PR	PR	30-DEC-1999; 99WO-US0031274.	
PR	PR	18-FEB-2000; 2000WO-US004341.	
PR	PR	01-MAR-2000; 2000WO-US005601.	
PR	PR	02-MAR-2000; 2000WO-US005841.	
PR	PR	21-MAR-2000; 2000WO-US007532.	
PR	PR	22-MAY-2000; 2000WO-US014042.	
PR	PR	02-JUN-2000; 2000WO-US015264.	
PR	PR	22-AUG-2000; 2000US-00644848.	
PR	PR	24-AUG-2000; 2000WO-US023328.	
PR	PR	18-SEP-2000; 2000US-00664610.	
PR	PR	18-SEP-2000; 2000US-00665350.	
PR	PR	08-NOV-2000; 2000US-00709238.	
PR	PR	10-NOV-2000; 2000WO-US030873.	
PR	PR	01-DEC-2000; 2000WO-US032678.	
PR	PR	20-DEC-2000; 2000US-00747259.	
PR	PR	20-DEC-2000; 2000WO-US034956.	
PR	PR	28-FEB-2001; 2001WO-US006520.	
PR	PR	22-MAR-2001; 2001US-00816744.	
PR	PR	10-MAY-2001; 2001US-00854208.	
PR	PR	10-MAY-2001; 2001US-00854280.	
PR	PR	30-MAY-2001; 2001US-00870574.	
PR	PR	01-JUN-2001; 2001WO-US017800.	
PR	PR	05-JUN-2001; 2001US-00874503.	
PR	PR	29-JUN-2001; 2001US-00869599.	
PR	PR	18-JUL-2001; 2001US-00908827.	
PR	PR	06-DEC-2001; 2001US-00008867.	
XX	XX	(GETH) GENENTECH INC.	
XX	XX	Raton DL, Pilyaroff B, Gerritsen ME, Goddard A, Godowski PJ;	
PI	PI	Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;	
XX	XX	N-PSDB; ACH66306.	
DR	DR	WPI; 2003-456358/43.	
XX	XX	PRO polypeptide, useful for preparing a medicament for treating a	
PT	PT	condition associated with PRO polypeptide.	
XX	XX	Disclosure; Fig 126; 222pp; English.	
XX	XX	The invention describes an isolated polypeptide having at least 80, 85,	
CC	CC	90, 95 or 99% identity with: (a) a sequence having 46-335 amino acids, or	
CC	CC	its extracellular domain; (b) a sequence having 46-335 amino acids,	
CC	CC	lacking its associated signal peptide; or (c) an amino acid sequence	
CC	CC	encoded by the full-length coding sequence of the cDNA (ATCC accession	
CC	CC	number 209956). The PRO (secreted and transmembrane) polypeptide is	
CC	CC	useful for preparing a medicament for treating a condition associated	
CC	CC	with PRO polypeptide. This is the amino acid sequence of a novel human	
CC	CC	secreted and transmembrane PRO polypeptide	
XX	XX	SQ Sequence 323 AA;	
Query Match 100.0%; Score 1690; DB 6; Length 323;			
Best Local Similarity 100.0%; Pred. No. 2e-165;			
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MSVPEEEERLLPLTORWPRASKFLLSGCAATVAELATFFLDLTTRLQMGEEAALARLGD	60
Db	1	MSVPEEEERLLPLTORWPRASKFLLSGCAATVAELATFFLDLTTRLQMGEEAALARLGD	60
Qy	61	GARESAFYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYEHLEWVFGKS	120
Db	61	GARESAFYRGWVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGRMVYEHLEWVFGKS	120
Qy	121	EDEHYPLWKSIVIGMMAGVIGQFLANPTDLVKVQOMEGKRLKLGKPLRPRGVHHAFAKI	180
Db	121	EDEHYPLWKSIVIGMMAGVIGQFLANPTDLVKVQOMEGKRLKLGKPLRPRGVHHAFAKI	180
Qy	181	LAEGGIRGLWAGWVPNIQRAALVNMGDLTYYDTVKHYLVNLTPLEDNIMTHGLSSLCSGL	240
Db	181	LAEGGIRGLWAGWVPNIQRAALVNMGDLTYYDTVKHYLVNLTPLEDNIMTHGLSSLCSGL	240
Qy	241	VASILGTPADVIKSRIMNQPRDKQGRGLLYKSTDCCLIQAVQEGFMSLYKGLPWSLWRM	300
Db	241	VASILGTPADVIKSRIMNQPRDKQGRGLLYKSTDCCLIQAVQEGFMSLYKGLPWSLWRM	300
Qy	301	TPWSMVFWLTYEKIREMSGVSPF 323	
Db	301	TPWSMVFWLTYEKIREMSGVSPF 323	
Search completed: September 24, 2004, 03:52:16			
Job time: 100 secs			

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2004, 03:51:03 ; Search time 51 Seconds
(without alignments)
326.964 Million cell updates/sec

Title: US-09-397-342C-1

Perfect score: 1690

Sequence: 1 MSVPBEEERLLPTQWRPA.....SMVFWLTYKIREMSGVSPF 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A COMB.pdp.*

2: /cgn2_6/ptodata/2/iaa/5B COMB.pdp.*

3: /cgn2_6/ptodata/2/iaa/6A COMB.pdp.*

4: /cgn2_6/ptodata/2/iaa/6B COMB.pdp.*

5: /cgn2_6/ptodata/2/iaa/PTUS COMB.pdp.*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	560	33.1	291	4	US-09-501-558-2
2	557.5	33.0	290	4	US-09-743-847-2
3	557.5	33.0	335	4	US-09-482-273-118
4	476.5	28.2	309	4	US-10-001-051B-2
5	475.5	28.1	312	3	US-09-142-565-2
6	475.5	28.1	312	4	US-09-808-457-2
7	475.5	28.1	312	4	US-09-423-410-4
8	473.5	28.0	309	4	US-09-743-847-4
9	472.5	28.0	299	1	US-08-518-878B-56
10	472.5	28.0	299	2	US-08-470-868A-56
11	472.5	28.0	309	1	US-08-518-878B-51
12	472.5	28.0	309	2	US-08-807-861A-51
13	472.5	28.0	309	2	US-08-470-868A-51
14	472.5	28.0	309	3	US-09-210-681-51
15	472.5	28.0	309	3	US-08-946-719A-51
16	472.5	28.0	309	4	US-09-547-983-51
17	472.5	28.0	432	2	US-08-937-466-4
18	472.5	28.0	432	2	US-09-172-528-4
19	472.5	28.0	432	3	US-09-318-199-4
20	472.5	28.0	432	3	US-09-503-579-4
21	469.5	27.8	308	2	US-08-937-466-2
22	469.5	27.8	308	2	US-09-172-528-2
23	469.5	27.8	308	3	US-09-318-199-2
24	469.5	27.8	308	3	US-09-503-579-2
25	466.5	27.6	310	4	US-09-743-847-5
26	447.5	26.5	307	4	US-09-743-847-3
27	440	26.0	293	4	US-09-501-558-4

28	439	26.0	306	5	PCT-US94-09799-1	Sequence 1, Appli
29	424	25.1	307	2	US-08-807-861A-56	Sequence 56, Appl
30	424	25.1	307	3	US-09-210-681-56	Sequence 56, Appl
31	424	25.1	307	3	US-08-946-719A-56	Sequence 56, Appl
32	424	25.1	307	4	US-09-547-983-56	Sequence 56, Appl
33	404.5	23.9	275	4	US-09-808-457-4	Sequence 4, Appli
34	404.5	23.9	275	4	US-09-423-410-6	Sequence 6, Appli
35	396.5	23.5	303	1	US-08-518-878B-37	Sequence 37, Appl
36	396.5	23.5	303	1	US-08-294-522B-36	Sequence 36, Appl
37	396.5	23.5	303	2	US-08-807-861A-37	Sequence 37, Appl
38	396.5	23.5	303	2	US-08-470-868A-37	Sequence 37, Appl
39	396.5	23.5	303	3	US-09-210-681-37	Sequence 37, Appl
40	396.5	23.5	303	3	US-08-946-719A-37	Sequence 37, Appl
41	396.5	23.5	303	4	US-09-547-983-37	Sequence 37, Appl
42	376.5	22.3	256	2	US-08-937-466-6	Sequence 6, Appli
43	376.5	22.3	256	2	US-09-172-528-6	Sequence 6, Appli
44	376.5	22.3	256	3	US-09-318-199-6	Sequence 6, Appli
45	376.5	22.3	256	3	US-09-503-579-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-501-558-2
; Sequence 2, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6403784el Human Uncoupling Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0012-USA
; CURRENT APPLICATION NUMBER: US/09/501,558
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-501-558-2

Query Match	33.1%;	Score 560;	DB 4;	Length 291;
Best Local Similarity	39.0%;	Pred. No. 4.4e-52;		
Matches 115;	Conservative 62;	Mismatches 104;	Indels 14;	Gaps 4;
QY	23	FLLSGCAATVAELATPPLDLTKRLQMQGEAALRLDGDGARESPYRGVMVRLTGITEEE	82	
Db	9	FVYGGASITABCGTFPDLTKRLIQQT-----NDAKFKIRYRGLHALVRIGREE	63	
QY	83	GFLLMQGVTPAIYRHVYSGGRMVTYEHRLREVFOKSEDEHYPLMKSVTGMWAGVIGQ	142	
Db	64	GLKALYSIAPAMLRQASGTIKIGYQSLKRLFIERPEDETLPI--NVICGLSGVISS	121	
QY	143	FLANPTDLVKVQOMEGKLECKPLRFVGVHFAKILAEGGIRGLWAGVNPVNOAAL	202	
Db	122	TIANPTDLVKIRMQAQ--SNTIQG-----GMIGNFMNIYQOEGTRGLWKGVSUTAQAAL	174	
QY	203	VNMGDLITTYDVGVHYLVNLTPTEDNIMTHGLSLCSGLVASILGTADVIKSRIMNOPRD	262	
Db	175	VVGVELPVVDIYTKHLLSLGMDTVYTHFLSSFTCLAGALASNPVDVVRTRMNOVL	234	
QY	263	KQGRGLLYKSSDCLIQAVQGGFMSLYKGFIPSWLRMTFWSMVFWLTYEKIREM	317	
Db	235	RDGRCSGYTGLDCLIQTKWNEGFALYKGFNPWLRLGPNWIIFFVYBQLKKL	289	

RESULT 2
US-09-743-847-2
; Sequence 2, Application US/09743847

```
; Patent No. 6602694
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Albrandt, Keith
; APPLICANT: Beaumont, Kevin
; APPLICANT: Young, Andrew
; TITLE OF INVENTION: UNCOUPLIN PROTEIN 4 (UCP-4) AND METHODS OF USE
; FILE REFERENCE: 235/108_0026
; CURRENT APPLICATION NUMBER: US/09/743,847
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/092,737
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: PCT/US99/15861
; PRIOR FILING DATE: 1999-07-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-743-847-2

Query Match      33.0%; Score 557.5; DB 4; Length 290;
Best Local Similarity 39.9%; Pred. No. 8.1e-52;
Matches 118; Conservative 63; Mismatches 98; Indels 17; Gaps 5;

Qy 23 FLISGCAATVAELATPFLDLTKTRLQMGGAALRLGDGAREGAPYRGWRTALGIIEEE 82
Db 9 FVYGGSLASIVAEFGTFPVDLTKTRLQVQGSIDARF-----KEIKYRGMPHALFRICKEE 63

Qy 83 GFLKLMQGVTPAIRVHVYSGRMVTVYHLREVVFSGSEDEHYPLWKSIVGGMMAGVIGQ 142
Db 64 GVLALYSGIAPALLRQASGTIKIGIYQSLKRLFVERLEDE--TLINMICGVVGVSS 121

Qy 143 FLANPTDLVKVQMGEGKRLKGLKPLFRFG-VHFAFAKILAEGGIRGLWAGVVPNIQRAA 201
Db 122 TIANPTDLVKIRMQAQS-----LFQSGMISGFDIYQEGTRGLWGVVPTAQRAA 173

Qy 202 LVNMGDLTYYTVKHYLVNTPLEDNIMTHGLSSGLVASILGTPADVIKSRIMNQR 261
Db 174 IVGVVELPVYDITKHLILSGMMGDTILTHFVSSFTCGLAGALASNPVDVTRMMNQ-R 232

Qy 262 DKQGRGLLYKSSDCLIQAVQGGFMSLYKGLPLSLRMT-PWSMVFWLTVEKIREM 317
Db 233 AIVGHVDLYKGTVDGILKMKWKHEGFFALYKGFNPWNLRLGPNWLIIFITTEYQLKRL 288

RESULT 3
US-09-482-273-118
; Sequence 118, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; CURRENT FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 118
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE

; LOCATION: (335)
; OTHER INFORMATION: Xaa equals stop translation
; US-09-482-273-118

Query Match      33.0%; Score 557.5; DB 4; Length 335;
Best Local Similarity 39.9%; Pred. No. 1e-51;
Matches 118; Conservative 63; Mismatches 98; Indels 17; Gaps 5;

Qy 23 FLISGCAATVAELATPFLDLTKTRLQMGGAALRLGDGAREGAPYRGWRTALGIIEEE 82
Db 53 FVYGGSLASIVAEFGTFPVDLTKTRLQVQGSIDARF-----KEIKYRGMPHALFRICKEE 107

Qy 83 GFLKLMQGVTPAIRVHVYSGRMVTVYHLREVVFSGSEDEHYPLWKSIVGGMMAGVIGQ 142
Db 108 GVLALYSGIAPALLRQASGTIKIGIYQSLKRLFVERLEDE--TLINMICGVVGVSS 165

Qy 143 FLANPTDLVKVQMGEGKRLKGLKPLFRFG-VHFAFAKILAEGGIRGLWAGVVPNIQRAA 201
Db 166 TIANPTDLVKIRMQAQS-----LFQSGMISGFDIYQEGTRGLWGVVPTAQRAA 217

Qy 202 LVNMGDLTYYTVKHYLVNTPLEDNIMTHGLSSGLVASILGTPADVIKSRIMNQR 261
Db 218 IVGVVELPVYDITKHLILSGMMGDTILTHFVSSFTCGLAGALASNPVDVTRMMNQ-R 276

Qy 262 DKQGRGLLYKSSDCLIQAVQGGFMSLYKGLPLSLRMT-PWSMVFWLTVEKIREM 317
Db 277 AIVGHVDLYKGTVDGILKMKWKHEGFFALYKGFNPWNLRLGPNWLIIFITTEYQLKRL 332

RESULT 4
US-10-001-051B-2
; Sequence 2, Application US/10001051B
; Patent No. 6670138
; GENERAL INFORMATION:
; APPLICANT: Gonzalez-Zulueta, Mirella
; APPLICANT: Shamloo, Mehrdad
; APPLICANT: McFarland, K.C.
; APPLICANT: Chin, Daniel
; APPLICANT: Wielech, Tadeusz
; APPLICANT: Melcher, Thorsten
; APPLICANT: AGY Therapeutics, Inc.
; TITLE OF INVENTION: METHODS OF DIAGNOSING , PREVENTING AND TREATING
; FILE REFERENCE: 019488-003010US
; CURRENT APPLICATION NUMBER: US/10/001,051B
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/244,946
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Any animal
; OTHER INFORMATION: source, typically mammalian, most typically human
; US-10-001-051B-2

Query Match      28.2%; Score 476.5; DB 4; Length 309;
Best Local Similarity 34.4%; Pred. No. 5e-43;
Matches 104; Conservative 66; Mismatches 111; Indels 21; Gaps 6;

Qy 18 PRAS-KFLISGCAATVAELATPFLDLTKTRLQMGGAALRLGDG---ARESAPYRGWVR 73
Db 11 PTATVKFLGAGTAACIADLTTPDLDTAKVRLQIGES-----QGFVRATASQYRGVMG 64

Qy 74 TALGIIIEEGFLKMQGVTPAIRVHVYSGRMVTVYHLREVVFSGSEDEHYPLWKSIVG 133
Db 65 TILTVRTGPRSLYNGLVAGLQRMSPASVRIGLYDSVKQ--FYTKGEHASIGSRLLA 122

Qy 134 GMMAGVIGQLANPTDLVKVQMGEGKRLKGLKPLFRFGVHFAFAKILAEGGIRGLWAG 193
```

```
Db 123 GSTTGALAVAAQPTDVVKVFOAQR---AGGRRYQSTVNAYKTIAREEGRGLWKGT 179
QY 194 VPIQRAALVNMGDLTYDTVKHYLVNLTPLEDNIMTHGLSSLCGLVASILGTTPADVIK 253
Db 180 SPVNARNAIVNCAELTYDILKALKANLMTDLPCHFISAFGAGFCITVIASPDVVK 239
QY 254 SRIMNPRDKQGRGLYKSTDCCLIOAQVQEGFMSLYKGLPSWLRLMTPSWVFWLTVEK 313
Db 240 TRYMNSALGQ-----YSSAGHCALTWLQEGPRAPYKGMPSFLRLGSNVNVFVTEQ 293
QY 314 IR 315
Db 294 LK 295

RESULT 5
US-09-142-565-2
; Sequence 2, Application US/09142565A
; Patent No. 6187560
; GENERAL INFORMATION:
; APPLICANT: Lee James Beeley
; APPLICANT: Kelly Paine
; APPLICANT: Robert James
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30002
; CURRENT APPLICATION NUMBER: US/09/142,565A
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 9704551.2
; EARLIER FILING DATE: 1997-03-05
; EARLIER APPLICATION NUMBER: 9705614.7
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 97305305.1
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
; OTHER INFORMATION: Protein UCP3L
US-09-142-565-2

Query Match 28.1%; Score 475.5; DB 3; Length 312;
Best Local Similarity 35.8%; Pred. No. 6.5e-43;
Matches 113; Conservative 59; Mismatches 116; Indels 29; Gaps 7;

QY 20 ASKFLSGCAATVAELATFPDLTKTRLQOGE---AALARLGDGARESPYRGMTAL 76
Db 14 AVKFLGAGTAACPADLVTFPLDTAKVRLQIQENQAVQTARL-----VQYRGVLGTIL 66
QY 77 GIIEEGFLKMQGVTPAIYRHVVYSGRMVTVYHLEHVFGKSEDEHYPLWKSIVIGMM 136
Db 67 TWRTGEGPCSPYNGLVAGLQRMFSASIRIGLDSVKQVTPKQAD-NSSLTRILAGCT 125
QY 137 AGVIGQFLANPTDLVKVQMQE---GKRKLEGLRFRGVHAFKILAEGLGIRLWAGW 193
Db 126 TGAMAVTCAQPTDVVKVFOASIHGFSRSDRK---YSGTMDAVRTIAREEGVRLWKGT 182
QY 194 VPIQRAALVNMGDLTYDTVKHYLVNLTPLEDNIMTHGLSSLCGLVASILGTTPADVIK 253
Db 183 LPNIMRNAIVNCAEVVTDILKEKLDYHLLTDFPCHFVSFAFGAGFCATVWASPDVVK 242
QY 254 SRIMNPRDKQGRGLYKSTDCCLIOAQVQEGFMSLYKGLPSWLRLMTPSWVFWLTVEK 313
Db 243 TRYMNSPPGQ-----YFSPDLCMIKMWAOEGPTAFYKGTTPSFLRIGSNVNVFVTEQ 296
QY 314 IR-----EMSGVSPF 323
Db 297 LKRALMKVQMLRESPP 312

RESULT 6
US-09-142-565-2
; Sequence 2, Application US/09808457
; Patent No. 6187560
; GENERAL INFORMATION:
; APPLICANT: Lee James Beeley
; APPLICANT: Kelly Paine
; APPLICANT: Robert James
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30002
; CURRENT APPLICATION NUMBER: US/09/142,565A
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 9704551.2
; EARLIER FILING DATE: 1997-03-05
; EARLIER APPLICATION NUMBER: 9705614.7
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 97305305.1
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
; OTHER INFORMATION: Protein UCP3L
US-09-142-565-2

Query Match 28.1%; Score 475.5; DB 3; Length 312;
Best Local Similarity 35.8%; Pred. No. 6.5e-43;
Matches 113; Conservative 59; Mismatches 116; Indels 29; Gaps 7;

QY 20 ASKFLSGCAATVAELATFPDLTKTRLQOGE---AALARLGDGARESPYRGMTAL 76
Db 14 AVKFLGAGTAACPADLVTFPLDTAKVRLQIQENQAVQTARL-----VQYRGVLGTIL 66
QY 77 GIIEEGFLKMQGVTPAIYRHVVYSGRMVTVYHLEHVFGKSEDEHYPLWKSIVIGMM 136
Db 67 TWRTGEGPCSPYNGLVAGLQRMFSASIRIGLDSVKQVTPKQAD-NSSLTRILAGCT 125
QY 137 AGVIGQFLANPTDLVKVQMQE---GKRKLEGLRFRGVHAFKILAEGLGIRLWAGW 193
Db 126 TGAMAVTCAQPTDVVKVFOASIHGFSRSDRK---YSGTMDAVRTIAREEGVRLWKGT 182
QY 194 VPIQRAALVNMGDLTYDTVKHYLVNLTPLEDNIMTHGLSSLCGLVASILGTTPADVIK 253
Db 183 LPNIMRNAIVNCAEVVTDILKEKLDYHLLTDFPCHFVSFAFGAGFCATVWASPDVVK 242
QY 254 SRIMNPRDKQGRGLYKSTDCCLIOAQVQEGFMSLYKGLPSWLRLMTPSWVFWLTVEK 313
Db 243 TRYMNSPPGQ-----YFSPDLCMIKMWAOEGPTAFYKGTTPSFLRIGSNVNVFVTEQ 296
QY 314 IR-----EMSGVSPF 323
Db 297 LKRALMKVQMLRESPP 312

RESULT 6
US-09-142-565-2
; Sequence 2, Application US/09808457
; Patent No. 6187560
; GENERAL INFORMATION:
; APPLICANT: Lee James Beeley
; APPLICANT: Kelly Paine
; APPLICANT: Robert James
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30002
; CURRENT APPLICATION NUMBER: US/09/142,565A
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 9704551.2
; EARLIER FILING DATE: 1997-03-05
; EARLIER APPLICATION NUMBER: 9705614.7
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 97305305.1
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
; OTHER INFORMATION: Protein UCP3L
US-09-142-565-2

Query Match 28.1%; Score 475.5; DB 4; Length 312;
Best Local Similarity 35.8%; Pred. No. 6.5e-43;
Matches 113; Conservative 58; Mismatches 116; Indels 29; Gaps 7;

QY 20 ASKFLSGCAATVAELATFPDLTKTRLQOGE---AALARLGDGARESPYRGMTAL 76
Db 14 AVKFLGAGTAACPADLVTFPLDTAKVRLQIQENQAVQTARL-----VQYRGVLGTIL 66
QY 77 GIIEEGFLKMQGVTPAIYRHVVYSGRMVTVYHLEHVFGKSEDEHYPLWKSIVIGMM 136
Db 67 TWRTGEGPCSPYNGLVAGLQRMFSASIRIGLDSVKQVTPKQAD-NSSLTRILAGCT 125
QY 137 AGVIGQFLANPTDLVKVQMQE---GKRKLEGLRFRGVHAFKILAEGLGIRLWAGW 193
Db 126 TGAMAVTCAQPTDVVKVFOASIHGFSRSDRK---YSGTMDAVRTIAREEGVRLWKGT 182
QY 194 VPIQRAALVNMGDLTYDTVKHYLVNLTPLEDNIMTHGLSSLCGLVASILGTTPADVIK 253
Db 183 LPNIMRNAIVNCAEVVTDILKEKLDYHLLTDFPCHFVSFAFGAGFCATVWASPDVVK 242
QY 254 SRIMNPRDKQGRGLYKSTDCCLIOAQVQEGFMSLYKGLPSWLRLMTPSWVFWLTVEK 313
Db 243 TRYMNSPPGQ-----YFSPDLCMIKMWAOEGPTAFYKGTTPSFLRIGSNVNVFVTEQ 296
QY 314 IR-----EMSGVSPF 323
Db 297 LKRALMKVQMLRESPP 312

RESULT 7
US-09-423-410-4
; Sequence 4, Application US/09423410
; Patent No. 6620594
; GENERAL INFORMATION:
; APPLICANT: Giacobino, Jean-Paul
; APPLICANT: Muzzin, Patrick
; APPLICANT: Boss, Olivier
; TITLE OF INVENTION: UNCOUPLING PROTEIN HOMOLOGUE: UCP3
; FILE REFERENCE: 4-30353/A
; CURRENT APPLICATION NUMBER: US/09/423,410
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: PCT/EP98/02645
; EARLIER FILING DATE: 1998-05-05
; EARLIER APPLICATION NUMBER: 1072/97
; EARLIER FILING DATE: 1997-05-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
```

```
; Patent No. 6608038
; GENERAL INFORMATION:
; APPLICANT: Boettcher, Brian
; APPLICANT: Caplan, Shari
; APPLICANT: Kaleko, Michael
; APPLICANT: Connelly, Shelia
; APPLICANT: Desai, Urvi
; APPLICANT: Slosberg, Eric
; TITLE OF INVENTION: Methods and Compositions For Treatment
; OF Diabetes and Related Conditions Via Gene Therapy
; FILE REFERENCE: 4-31353A/USN
; CURRENT APPLICATION NUMBER: US/09/808,457
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/xxx,xxx
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Protein UCP3L
US-09-808-457-2

Query Match 28.1%; Score 475.5; DB 4; Length 312;
Best Local Similarity 35.8%; Pred. No. 6.5e-43;
Matches 113; Conservative 58; Mismatches 116; Indels 29; Gaps 7;

QY 20 ASKFLSGCAATVAELATFPDLTKTRLQOGE---AALARLGDGARESPYRGMTAL 76
Db 14 AVKFLGAGTAACPADLVTFPLDTAKVRLQIQENQAVQTARL-----VQYRGVLGTIL 66
QY 77 GIIEEGFLKMQGVTPAIYRHVVYSGRMVTVYHLEHVFGKSEDEHYPLWKSIVIGMM 136
Db 67 TWRTGEGPCSPYNGLVAGLQRMFSASIRIGLDSVKQVTPKQAD-NSSLTRILAGCT 125
QY 137 AGVIGQFLANPTDLVKVQMQE---GKRKLEGLRFRGVHAFKILAEGLGIRLWAGW 193
Db 126 TGAMAVTCAQPTDVVKVFOASIHGFSRSDRK---YSGTMDAVRTIAREEGVRLWKGT 182
QY 194 VPIQRAALVNMGDLTYDTVKHYLVNLTPLEDNIMTHGLSSLCGLVASILGTTPADVIK 253
Db 183 LPNIMRNAIVNCAEVVTDILKEKLDYHLLTDFPCHFVSFAFGAGFCATVWASPDVVK 242
QY 254 SRIMNPRDKQGRGLYKSTDCCLIOAQVQEGFMSLYKGLPSWLRLMTPSWVFWLTVEK 313
Db 243 TRYMNSPPGQ-----YFSPDLCMIKMWAOEGPTAFYKGTTPSFLRIGSNVNVFVTEQ 296
QY 314 IR-----EMSGVSPF 323
Db 297 LKRALMKVQMLRESPP 312

RESULT 7
US-09-423-410-4
; Sequence 4, Application US/09423410
; Patent No. 6620594
; GENERAL INFORMATION:
; APPLICANT: Giacobino, Jean-Paul
; APPLICANT: Muzzin, Patrick
; APPLICANT: Boss, Olivier
; TITLE OF INVENTION: UNCOUPLING PROTEIN HOMOLOGUE: UCP3
; FILE REFERENCE: 4-30353/A
; CURRENT APPLICATION NUMBER: US/09/423,410
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: PCT/EP98/02645
; EARLIER FILING DATE: 1998-05-05
; EARLIER APPLICATION NUMBER: 1072/97
; EARLIER FILING DATE: 1997-05-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
```

```
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Protein UCP3L
US-09-423-410-4

Query Match      28.1%; Score 475.5; DB 4; Length 312;
Best Local Similarity 35.8%; Pred. No. 6.5e-43;
Matches 113; Conservative 58; Mismatches 116; Indels 29; Gaps 7;

QY 20 ASKFLSGCAATVAELATFPDLTKTLQMQGE---AALARLGDGARESAPIYRGVMTAL 76
Db 14 AVKFLGAGTAACFADLVTFPDLTKVRLQIQENQAQVQIARL-----VQYRGVLGTL 66

QY 77 GIIEBEGFLKMQGVTPAIRHVHVSGRMVTYHLREVVFSGKSEDEHYPLWKSIVIGMM 136
Db 67 TMVTEGPCSPYNGVLVAGLQRMFSASIRIGLYDSVKQVTPKGAD-NSSLTTRILAGCT 125

QY 137 AGVIGQFLANPTDLVKVQMQME---GKRLGKPLRFRGVHHAFAKILAEGRGLWAGW 193
Db 126 TGAWAVTCAQPTDVVKVRFQASIHLSGSRDRK---YSGTMDAYRTIAREEGVRLWKGT 182

QY 194 VPNIQRAALVNMGDLTYYTVKHVYLVNTPLEDNIMTHGLSSLCGLVASILGTPADVIK 253
Db 183 LPNIMRNAIVNCAEVYTDILKEKLLDYHLLTDFNPFCHVFSAGAGFCATVVASPVDVVK 242

QY 254 SRIMNQRDKQGRGLLYKSTDCLIQAVQGEQPMGLYKGLPDLPSLWMTWPMVFWLTYEK 313
Db 243 TRYMNSPPGQ-----YFSPLDCKMVAQEGPTAFYKGFPTSPFLRLGSMNVVMFVTEQ 296

QY 314 IR-----EMSGVSPF 323
Db 297 LKRALMKVQMLRESPP 312

RESULT 8
US-09-743-847-4
; Sequence 4, Application US/09743847
; Patent No. 6602694
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Albrandt, Keith
; APPLICANT: Beaumont, Kevin
; APPLICANT: Young, Andrew
; TITLE OF INVENTION: UNCOUPLIN PROTEIN 4 (UCP-4) AND METHODS OF USE
; FILE REFERENCE: 235/108.0026
; CURRENT APPLICATION NUMBER: US/09/743,847
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/092,737
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: PCT/US99/15861
; PRIOR FILING DATE: 1999-07-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-743-847-4

Query Match      28.0%; Score 473.5; DB 4; Length 309;
Best Local Similarity 34.4%; Pred. No. 1e-42;
Matches 104; Conservative 65; Mismatches 112; Indels 21; Gaps 6;

QY 18 PRAS-KFLLSGCAATVAELATFPDLTKTLQMQGEAALARLGDG---ARESAPIYRGVMT 73
Db 11 PTATVKEFLGAGTAACIADLTITPDLTKVRLQIQGES-----QGPVATASQYRGVMG 64

QY 74 TALGIIEBEGFLKMQGVTPAIRHVHVSGRMVTYHLREVVFSGKSEDEHYPLWKSIVIG 133
Db 65 TILTMVTEGPRSLYNGVLVAGLQRMFSASVIRIGLYDSVKQ--FYTKGSEHAGISGRLLA 122

QY 134 GMVAGVIGFLANPTDLVKVQMQMEGKRLGKPLRFRGVHHAFAKILAEGRGLWAGW 193
Db 113 GSTTGALAVAVAOPTDVVKVRFQAOAR---AGGRRYQSTVNAVYKTIAREEGVRLWKGT 169

; LENGTH: 312
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Protein UCP3L
US-09-423-410-4

Query Match      28.1%; Score 475.5; DB 4; Length 312;
Best Local Similarity 35.8%; Pred. No. 6.5e-43;
Matches 113; Conservative 58; Mismatches 116; Indels 29; Gaps 7;

QY 20 ASKFLSGCAATVAELATFPDLTKTLQMQGE---AALARLGDGARESAPIYRGVMTAL 76
Db 14 AVKFLGAGTAACFADLVTFPDLTKVRLQIQENQAQVQIARL-----VQYRGVLGTL 66

QY 77 GIIEBEGFLKMQGVTPAIRHVHVSGRMVTYHLREVVFSGKSEDEHYPLWKSIVIGMM 136
Db 67 TMVTEGPCSPYNGVLVAGLQRMFSASIRIGLYDSVKQVTPKGAD-NSSLTTRILAGCT 125

QY 137 AGVIGQFLANPTDLVKVQMQME---GKRLGKPLRFRGVHHAFAKILAEGRGLWAGW 193
Db 126 TGAWAVTCAQPTDVVKVRFQASIHLSGSRDRK---YSGTMDAYRTIAREEGVRLWKGT 182

QY 194 VPNIQRAALVNMGDLTYYTVKHVYLVNTPLEDNIMTHGLSSLCGLVASILGTPADVIK 253
Db 183 LPNIMRNAIVNCAEVYTDILKEKLLDYHLLTDFNPFCHVFSAGAGFCATVVASPVDVVK 242

QY 254 SRIMNQRDKQGRGLLYKSTDCLIQAVQGEQPMGLYKGLPDLPSLWMTWPMVFWLTYEK 313
Db 243 TRYMNSPPGQ-----YFSPLDCKMVAQEGPTAFYKGFPTSPFLRLGSMNVVMFVTEQ 296

QY 314 IR-----EMSGVSPF 323
Db 297 LKRALMKVQMLRESPP 312

RESULT 8
US-09-743-847-4
; Sequence 4, Application US/09743847
; Patent No. 6602694
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Albrandt, Keith
; APPLICANT: Beaumont, Kevin
; APPLICANT: Young, Andrew
; TITLE OF INVENTION: UNCOUPLIN PROTEIN 4 (UCP-4) AND METHODS OF USE
; FILE REFERENCE: 235/108.0026
; CURRENT APPLICATION NUMBER: US/09/743,847
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/092,737
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: PCT/US99/15861
; PRIOR FILING DATE: 1999-07-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-743-847-4

Query Match      28.0%; Score 473.5; DB 4; Length 309;
Best Local Similarity 34.4%; Pred. No. 1e-42;
Matches 104; Conservative 65; Mismatches 112; Indels 21; Gaps 6;

QY 18 PRAS-KFLLSGCAATVAELATFPDLTKTLQMQGEAALARLGDG---ARESAPIYRGVMT 73
Db 11 PTATVKEFLGAGTAACIADLTITPDLTKVRLQIQGES-----QGPVATASQYRGVMG 64

QY 74 TALGIIEBEGFLKMQGVTPAIRHVHVSGRMVTYHLREVVFSGKSEDEHYPLWKSIVIG 133
Db 65 TILTMVTEGPRSLYNGVLVAGLQRMFSASVIRIGLYDSVKQ--FYTKGSEHAGISGRLLA 122

QY 134 GMVAGVIGFLANPTDLVKVQMQMEGKRLGKPLRFRGVHHAFAKILAEGRGLWAGW 193
Db 113 GSTTGALAVAVAOPTDVVKVRFQAOAR---AGGRRYQSTVNAVYKTIAREEGVRLWKGT 169
```

194 VPNIQRAALVNMGLTDTYDVKHVLNTPLEDNIMTHGLSSLCGLVASILGTPADVIK 253
 170 SPVARNAINVCAELTYDLIKDALLKANLMTDLPCHFTSAFGAGCTTIVIASPVDVVK 229
 254 SRIMNPRDKQGRGLLYKSTDCLIQAVQEGGMSLYKGLPGLSWLRMTWPMWVFWLTYEK 313
 230 TRYMSALGO-----YSSAGHCALTWLOKEGPRAFYKGFMPFLRLGSMNVVWFVTEQ 283
 314 IR 315
 284 LK 285

RESULT 10
 US-08-470-868A-56
 ; Sequence 56, Application US/08470868A
 ; Patent No. 5861485
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis C.
 ; TITLE OF INVENTION: Compositions and Methods for the
 ; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie and Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/470,868A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-0031-999
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864
 ; TELEX: 66441 PENNIE
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 299 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; US-08-470-868A-56

Query Match 28.0%; Score 472.5; DB 2; Length 299;
 Best Local Similarity 34.4%; Pred. No. 1.3e-42;
 Matches 104; Conservative 65; Mismatches 112; Indels 21; Gaps 6;
 18 PRAS-KFLSLGCAATVAELATPDLTKRLQWQGEAALRLDGDG---ARESAPYRGVMR 73
 1 PTATVFLGAGTAACIADLTLPDLTKAVRLQIQGES-----QGPVATVSAQYRGVMG 54
 74 TALGIIEEGFLKLMQGVTPAIYRVHVYSGGRMVTYHLREVVFSGSEDEHYPLWKSIVG 133
 55 TILTVRTEGPRSLYGLVAGLQRMSPASVRIGLYDSVKQ--FYTKGSEHASIGSRLLA 112
 134 GMMAGVIGQFLANPTDLVKVQWQMEGRKLEKPLRFRGVHHAFAKILAEAGGIRGLWAGW 193
 113 GSTTGALAVAVAQPTDVVKVRFQAQAR---AGGRRYQSTVNAVYKTIAREEGFRGLWKGT 169
 194 VPNIQRAALVNMGLTDTYDVKHVLNTPLEDNIMTHGLSSLCGLVASILGTPADVIK 253

170 SPVARNAINVCAELTYDLIKDALLKANLMTDLPCHFTSAFGAGCTTIVIASPVDVVK 229
 254 SRIMNPRDKQGRGLLYKSTDCLIQAVQEGGMSLYKGLPGLSWLRMTWPMWVFWLTYEK 313
 230 TRYMSALGO-----YSSAGHCALTWLOKEGPRAFYKGFMPFLRLGSMNVVWFVTEQ 283
 314 IR 315
 284 LK 285

RESULT 11
 US-08-518-878B-51
 ; Sequence 51, Application US/08518878B
 ; Patent No. 5702902
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/518,878B
 ; FILING DATE: 23-AUG-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-036
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 309 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; US-08-518-878B-51

Query Match 28.0%; Score 472.5; DB 1; Length 309;
 Best Local Similarity 34.4%; Pred. No. 1.3e-42;
 Matches 104; Conservative 65; Mismatches 112; Indels 21; Gaps 6;
 18 PRAS-KFLSLGCAATVAELATPDLTKRLQWQGEAALRLDGDG---ARESAPYRGVMR 73
 11 PTATVFLGAGTAACIADLTLPDLTKAVRLQIQGES-----QGPVATVSAQYRGVMG 64
 74 TALGIIEEGFLKLMQGVTPAIYRVHVYSGGRMVTYHLREVVFSGSEDEHYPLWKSIVG 133
 65 TILTVRTEGPRSLYGLVAGLQRMSPASVRIGLYDSVKQ--FYTKGSEHASIGSRLLA 122
 134 GMMAGVIGQFLANPTDLVKVQWQMEGRKLEKPLRFRGVHHAFAKILAEAGGIRGLWAGW 193
 123 GSTTGALAVAVAQPTDVVKVRFQAQAR---AGGRRYQSTVNAVYKTIAREEGFRGLWKGT 179
 194 VPNIQRAALVNMGLTDTYDVKHVLNTPLEDNIMTHGLSSLCGLVASILGTPADVIK 253
 180 SPVARNAINVCAELTYDLIKDALLKANLMTDLPCHFTSAFGAGCTTIVIASPVDVVK 229
 254 SRIMNPRDKQGRGLLYKSTDCLIQAVQEGGMSLYKGLPGLSWLRMTWPMWVFWLTYEK 313

Db 240 TRYNSALGQ-----YSSAGHCALTMLOKEGPRAFYKGFPSFLRGLSNVNVFVYEQ 293

QY 314 IR 315
 :
 Db 294 LK 295

RESULT 12

US-08-807-861A-51
 ; Sequence 51, Application US/08807861A
 ; Patent No. 5853975
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis A.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
 ; TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/807,861A
 ; FILING DATE: 26-FEB-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/518,878
 ; FILING DATE: 23-AUG-1995
 ; APPLICATION NUMBER: US 08/470,868
 ; FILING DATE: 06-JUN-1995
 ; APPLICATION NUMBER: US 08/294,522
 ; FILING DATE: 23-AUG-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-066
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 309 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; US-08-807-861A-51

Query Match 28.0%; Score 472.5; DB 2; Length 309;
 Best Local Similarity 34.4%; Pred. No. 1.3e-42;
 Matches 104; Conservative 65; Mismatches 112; Indels 21; Gaps 6;

QY 18 PRAS-KFLSSGCAATVAELATPFLDLTKRLOMQGEAALRLGDG---ARESAPYRGWVR 73
 Db 11 PTATVKFLGAGTAACIADLTFFLDLTKAVRLQIQGES-----QGPVRATVSAQYRGVNG 64
 QY 74 TALGIIEEGFLKMGQVTPAIYRHVYSGRMVTVYHLREVVFGKSEDEHYPLWKSIVG 133
 Db 65 TILTWRTGEPRLSYNLVAGLQRMQSFASVRIGLYDSVKQ---FYTKGSEHASIGSRLLA 122
 QY 134 GNMAGVIGQFLANPTDLVKVQMQMEGKRLEKPLRFRGVHFAKILAEAGGIRGLWAGW 193
 Db 123 GSTTGALAVAVAQPTDVVKVRFQAQAR---AGGRRYQSTVNAYKTIAREEGFRGLWKGT 179
 QY 194 VPNIQRAALVNMGDLTYDVTVKHYLVNLTPLDNTIMTHGLSLCSGLVASILGTPADVIK 253

Db 180 SPNVARNAINVCAELTYDLDIKALLKANLMTDDLPCHFTSAFGAGFCTTVIASPVDVVK 239
 QY 254 SRIMNQPRDKQGRGLLYKSTDCLIQAVQGEFGMSLYKGLPGLSWLRMTWMSVFWLTYEK 313
 Db 240 TRYNSALGQ-----YSSAGHCALTMLOKEGPRAFYKGFPSFLRGLSNVNVFVYEQ 293
 QY 314 IR 315
 :
 Db 294 LK 295

RESULT 13

US-08-470-868A-51
 ; Sequence 51, Application US/08470868A
 ; Patent No. 5861485
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis C.
 ; TITLE OF INVENTION: Compositions and Methods for the
 ; TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie and Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/470,868A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-0031-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864
 ; TELEX: 66441 PENNIE
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 309 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; US-08-470-868A-51

Query Match 28.0%; Score 472.5; DB 2; Length 309;
 Best Local Similarity 34.4%; Pred. No. 1.3e-42;
 Matches 104; Conservative 65; Mismatches 112; Indels 21; Gaps 6;

QY 18 PRAS-KFLSSGCAATVAELATPFLDLTKRLOMQGEAALRLGDG---ARESAPYRGWVR 73
 Db 11 PTATVKFLGAGTAACIADLTFFLDLTKAVRLQIQGES-----QGPVRATVSAQYRGVNG 64
 QY 74 TALGIIEEGFLKMGQVTPAIYRHVYSGRMVTVYHLREVVFGKSEDEHYPLWKSIVG 133
 Db 65 TILTWRTGEPRLSYNLVAGLQRMQSFASVRIGLYDSVKQ---FYTKGSEHASIGSRLLA 122
 QY 134 GNMAGVIGQFLANPTDLVKVQMQMEGKRLEKPLRFRGVHFAKILAEAGGIRGLWAGW 193
 Db 123 GSTTGALAVAVAQPTDVVKVRFQAQAR---AGGRRYQSTVNAYKTIAREEGFRGLWKGT 179
 QY 194 VPNIQRAALVNMGDLTYDVTVKHYLVNLTPLDNTIMTHGLSLCSGLVASILGTPADVIK 253
 Db 180 SPNVARNAINVCAELTYDLDIKALLKANLMTDDLPCHFTSAFGAGFCTTVIASPVDVVK 239

QY 254 SRIMQPRDKQGRGLLYKSDCLIOAQVQEGFMSLYKGFLPSWLRLMTWMSVFWLTYEK 313
Db 240 TRYMSALQ-----YSSAGHCHALTMLOKEGPRAFYKGFMPFSLRGLGSNNVVMFVTEYQ 293
QY 314 IR 315
Db 294 LK 295

RESULT 14
US-09-210-681-51
; Sequence 51, Application US/09210681
; Patent No. 6057109
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/807,861
; FILING DATE: 26-FEB-1997
; APPLICATION NUMBER: US 08/518,878
; FILING DATE: 23-AUG-1995
; APPLICATION NUMBER: US 08/470,868
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/294,522
; FILING DATE: 23-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; US-09-210-681-51

Query Match 28.0%; Score 472.5; DB 3; Length 309;
Best Local Similarity 34.4%; Pred. No. 1.3e-42;
Matches 104; Conservative 65; Mismatches 112; Indels 21; Gaps 6;

QY 18 PRAS-KFLISGCAATVAELATPFLDLTKRLQMOGEAALARLGDG---ARESAPYGMVR 73
Db 11 PTATVKFLGAGTAACTADLITPFLDTAKVRLQIGSES-----QGPVRATVSAQYRGVMG 64
QY 74 TALGIIEEGFLKMGVTPAIYRHVVYSGRMVTVYHLRVVFGKSEDEHYPLWKSVMG 133
Db 65 TILTWRTTGPRLSYNLVAGLQRMSPASVRLGLYDSVKQ--FYTKGSEHASIGRLIA 122
QY 134 GMMAGVIGOFLANPTDLVKVQMOMEGKRLKGLRFRGVHFAKILAEGGIRGLWAGW 193

Db 123 GSTTGALAVAVAQPTDVVKRFOAQR---AGGRRYQSTVNAYKTIAREEGRGLWKGT 179
QY 194 VPIORAAALVNMGDLTTTYDTVKHYLVNTPLEBNDINMTHGLSSILCSGLVASILGTADVIK 253
Db 180 SPVARNALVNCALVTVYDLIKDALLKANLMTDDLPCFTSAFGAGCFTTVIASPVDVVK 239
QY 254 SRIMQPRDKQGRGLLYKSDCLIOAQVQEGFMSLYKGFLPSWLRLMTWMSVFWLTYEK 313
Db 240 TRYMSALQ-----YSSAGHCHALTMLOKEGPRAFYKGFMPFSLRGLGSNNVVMFVTEYQ 293
QY 314 IR 315
Db 294 LK 295

RESULT 15
US-08-946-719A-51
; Sequence 51, Application US/08946719A
; Patent No. 6121017
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,719A
; FILING DATE: 8-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/807,861
; FILING DATE: 26-FEB-1997
; APPLICATION NUMBER: US 08/518,878
; FILING DATE: 23-AUG-1995
; APPLICATION NUMBER: US 08/470,868
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/294,522
; FILING DATE: 23-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; US-08-946-719A-51

Query Match 28.0%; Score 472.5; DB 3; Length 309;
Best Local Similarity 34.4%; Pred. No. 1.3e-42;
Matches 104; Conservative 65; Mismatches 112; Indels 21; Gaps 6;

QY 18 PRAS-KFLISGCAATVAELATPFLDLTKRLQMOGEAALARLGDG---ARESAPYGMVR 73
Db 11 PTATVKFLGAGTAACTADLITPFLDTAKVRLQIGSES-----QGPVRATVSAQYRGVMG 64

```

QY 74 TALGIIIEEGFLKMOQVTPAIYRHVYVYSGRMVYEHLEVVVFGKSEDEHYPLWKS VIG 133
Db 65 TILTMVTEGPRSLYNGLVAGLQOMSFASVRIGLYDSVKQ--FYTKGSEHASIGSRLLA 122
QY 134 GMMAGVIGQFLANPTDLVKYQOMQMEGKRKLEGPRLPRGVHHAFAKILAEGGIRGLWAGW 193
Db 123 GSTTGALAVAVAQPTDVVKVRFQOAR---AGGRRYQSTVNAYKTIAREEGFRGLWKGT 179
QY 194 VPNIQRAALVNMGDLTTYDTVKHYLVLTNTPLEDNIMTHGLSLCSGLVASILGTADVIK 253
Db 180 SPNVARNAINVCAELVTYDUIKALLKANLMTDDLPCHFTSAFGAGFCITVIASPDVVK 239
QY 254 SRIMNQRDKQGRLLYKSSDCLIOAVQGEQFMSLYKGFPLPSWLMTWMSVFWLTYEK 313
Db 240 TRYMSALGO-----YSSAGHCALTWLQKEGPRAFYKGFMPSPFLRLGSMNVVMFVTEQ 293
QY 314 IR 315
Db 294 LK 295

```

Search completed: September 24, 2004, 03:58:35
Job time : 53 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2004, 03:44:32 ; Search time 49 Seconds
(without alignments)
634.079 Million cell updates

Title: US-09-397-342C-1
 Perfect score: 1690
 Sequence: 1 MSVPEEEERLLPLQRPRA.....SMVFNLTYEKIREMSGVSPF 323
 Scoring table: BLOSUM62
 Gapop 10.0 , Gabext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 2833366

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10
                  Listing first 45

```

```
Database : PTR_78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*
```

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	777	46.0	343	2	T15253	hypothetical prote
2	667.5	39.5	305	2	H86274	F7A19.22 protein -
3	551.5	32.6	325	2	JC7553	brain mitochondria
4	546.5	32.3	306	2	T47570	uncoupling protein
5	538.5	31.9	306	2	T07793	uncoupling protein
6	537.5	31.8	306	2	T52024	uncoupling protein
7	475.5	28.1	312	2	JC5522	uncoupling protein
8	455.5	27.0	313	2	D84613	hypothetical prote
9	447.5	26.5	307	2	G01858	uncoupling protein
10	434.5	25.7	306	2	A32446	uncoupling protein
11	432.5	25.6	313	2	T05577	uncoupling protein
12	425	25.1	307	2	S34268	uncoupling protein
13	424	25.1	306	2	A31106	mitochondrial unco
14	422	25.0	307	2	A26294	uncoupling protein
15	419.5	24.8	288	2	S03603	uncoupling protein
16	399.5	23.6	314	2	A36305	2-oxoglutarate/mal
17	387.5	22.9	314	2	A56650	car
18	381.5	22.6	323	2	T28459	hypothetical prote
19	366.5	21.7	290	2	S44091	oxoglutarate/malat
20	345	20.4	282	2	T49628	probable dicarboxy
21	338	20.0	298	2	S51351	hypothetical prote
22	333.5	19.7	324	2	S25357	mitochondrial unco
23	332	19.6	297	2	T07405	oxoglutarate/malat
24	299.5	17.7	302	2	S65042	2-oxoglutarate/mal
25	298	17.6	331	2	T51899	probable 2-oxoglut
26	296.5	17.5	302	2	S65040	2-oxoglutarate/mal
27	288	17.0	320	2	T37603	probable oxaloacet
28	272.5	16.1	352	2	T49156	hypothetical prote
29	269.5	15.9	359	2	T01729	mitochondrial solu

ALIGNMENTS

```

RESULT 1
T15253
hypothetical protein K07B1.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
C/Accession: T15253
R/Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, May 1997
A/Description: the sequence of C. elegans cosmid K07B1.
A/Reference number: Z18317
A/Accession: T15253
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-343 <PAU>
A/Cross-references: EMBL:AF003384; NID:G2088817; PID:G2088821; PIDN:AA85423
A/Experimental source: strain Bristol N2; clone K07B1
C/Genetics:
A/Gene: CESP:K07B1.3
A/Map position: 5
A/Introns: 81/1; 131/3; 236/3; 279/2
C/Superfamily: ADP.ATP carrier protein; ADP.ATP carrier protein repeat homo

```

RESULT 2

Db 183 LPNIMRNAIUNCBAVVTYDILKEKLDYLHLLTDFCHVFVSAPGAGFCATTVASPVDDVK 242

Qy 254 SRIMNPDRDKQGRLGLLYKSSTDCLIQAQOGEFGMSLYKGFLPSWLRTMPSWFMWTYRK 313
::|||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:

Db 243 TRYNSPPCG-----YFSPLCDMIKWAGEGTAFYKGFTSFLRGSNNVMVFITYEQ 296
::|||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:

Qy 314 IR-----EMSGVSPF 323
:: |:: |||

Db 297 LKRALKMQVLRES PF 312
:: |:: |||

RESULT 8
DB4613
hypothetical protein At2g22500 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-feb-2001 #text_change 16-Feb-2001
C;Accession: D84613
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
mus.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
E.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, G.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; UID:20083487; PMID:10617197
A;Accession: D84613
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-313 <S>
A;Cross-references: GB:AE002093; NID:g4544443; PIDN:AAD22351.1; GS PDB:GN00139
C;Genetics:
A;Gene: At2g22500
A;Map position: 2
C;Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

Query Match 27.0%; Score 455.5; DB 2; Length 313;
Best Local Similarity 34.7%; Pred. No. 1.1e-31;
Matches 107; Conservative 60; Mismatches 122; Indels 19; Gaps 6;

Qy 23 FLLGGCAATAVAELATFPDLTKTRLOMGEA-----ALARLGDGAESAPYR-GMV 72
:|||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:

Db 6 FAGGTASTAVAGCTHPDLLIKVRMLQSAPSPTQNLRPALAFQTSTVNAPPLRVGI 65
:|||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:

Qy 73 RTALGHIEEGFKLMGVTPTAIRHVVVYGGRMVVEHLREVVFGK---SEDEHYPLMK 129
:|||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:

Db 66 GVGRSLIREGMALPGSVSATLVRLTYLTSTRMGLY----DIKGEWTDPETKTWPLMK 121
:|||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:

Qy 130 SVTGGMWAGVIQLANPTDLVKVQMOMEKKLEGPFRGWHAFAKILAEGGIRGL 189
:|||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:

Db 122 KIGAGA TAGAIGA AVGNPADVPAMVYMQRADGLPLTDNR-NRYKSVLDITOMIRGEVTSL 180
:|||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:

Qy 190 WAGWNPNIORAALLNMGDLTTYDTVRHYLVNTPLEDNIMTHGLSSLCISGLVASII LGTPA 249
:|||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:

Db 181 WRGSSLTNRAMLVTSQLASYSVKETILEKLKDGLGTHVSASPAAFGVASVPNV 240
:|||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:

Qy 250 DVTKSRIMNOPRDQKRGRLLYKYSTDCCLIQAQOGEFGMSLYKGFLPSWLRTMPSWFMWFNL 309
:|||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:

Db 241 DVIKTRVMNW-KVGAVAPPYGAVDPKALTAKVKAEGIMSLSYKGFIP TVSRQAPTIVLFV 299
:|||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:: |:: |||:

Qy 310 TYEKIREM 317
|| :||||

Db 300 TLEQVKKL 307
|| :||||

RESULT 9
GO1858
uncoupling protein 1, mitochondrial - human
N;Alternate names: UCPI
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Jun-2000
C;Accession: GO1858; S78473; S29141; A60793; A45763
R;Bouillaud, F.
submitted to the EMBL Data Library, June 1995
A;Reference number: G08642
A;Accession: GO1858

RESULT 13

A31106
mitochondrial uncoupling protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jul-2000
C/Accession: A31106
R:Kozak, L.P.; Britton, J.H.; Kozak, U.C.; Wellis, J.M.
J. Biol. Chem. 263, 12274-12277, 1988
A:Title: The mitochondrial uncoupling protein gene. Correlation of exon structure to tra
A:Reference number: A31106, MUID:88315014; PMID:3410843
A:Accession: A31106
A:Molecule type: DNA; mRNA
A:Residues: 1-306 <KOZ>
A:Cross-references: GB:U63418; NID:g1519064; PID:AA807367.1; PID:g1519065
C:Genetics:
A:Gene: Ucp
A:Introns: 41/3; 108/1; 175/1; 209/1; 269/2
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; mitochondrion; transmembrane protein
F:9-102/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:109-201/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:208-295/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Search completed: September 24, 2004, 03:57:31
Job time : 50 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 23, 2004, 21:08:37 ; Search time 44 Seconds
(without alignments)
382.242 Million cell updates/sec

Title: US-09-397-342C-1

Perfect score: 1690

Sequence: 1 MSVPBEERLLPLTORPRA.....SMVFNLTYEKIREMSGVSPF 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1690	100.0	323	1 UCP4_HUMAN	O95847 homo sapien
2	557.5	33.0	325	1 UCP5_HUMAN	O95258 homo sapien
3	552.5	32.7	325	1 UCP5_MOUSE	O92252 mus musculus
4	504.5	29.9	311	1 UCP3_BOVIN	O77792 bos taurus
5	480.5	28.4	308	1 UCP3_PIG	O97649 sus scrofa
6	475.5	28.1	312	1 UCP3_HUMAN	P55916 homo sapien
7	474	28.0	311	1 UCP3_CANFA	O9219 canis famill
8	473.5	28.0	308	1 UCP3_MOUSE	P56501 mus musculus
9	473.5	28.0	309	1 UCP2_HUMAN	P55851 homo sapien
10	473.5	28.0	309	1 UCP2_RAT	P56500 rattus norv
11	472.5	28.0	309	1 UCP2_CANFA	O9219 canis famill
12	472.5	28.0	309	1 UCP2_MOUSE	P70406 mus musculus
13	472.5	28.0	309	1 UCP2_PIG	O97582 sus scrofa
14	471.5	27.9	308	1 UCP3_RAT	P56499 rattus norv
15	459	27.2	310	1 UCP2_CYPCA	O9W725 cyprinus ca
16	442	26.2	310	1 UCP2_BRARE	O9W720 brachydanio
17	441.5	26.1	307	1 UCP1_HUMAN	P25874 homo sapien
18	433.5	25.7	306	1 UCP1_RABIT	P14271 oryctolagus
19	425	25.1	306	1 UCP1_MESAU	P04575 mesocricetu
20	424	25.1	306	1 UCP1_MOUSE	P12242 mus musculus
21	422	25.0	306	1 UCP1_RAT	P04633 rattus norv
22	419.5	24.8	288	1 UCP1_BOVIN	P10861 bos taurus
23	399.5	23.6	313	1 M2OM_BOVIN	P22292 bos taurus
24	391.5	23.2	313	1 M2OM_MOUSE	O9C62 mus musculus
25	387.5	22.9	313	1 M2OM_HUMAN	O92978 homo sapien
26	376.5	22.3	313	1 M2OM_RAT	P97700 rattus norv
27	365	21.6	287	1 DIC_MOUSE	O9qz8 mus musculus
28	363	21.5	287	1 DIC_HUMAN	O9qbx3 homo sapien
29	333.5	19.7	324	1 OACI_YEAST	O21153 caenorhabdi
30	259	15.3	702	1 ODCI_YEAST	O21153 caenorhabdi
31	253	15.0	299	1 ODCI_CABEL	O9bq8 homo sapien
32	249.5	14.8	386	1 ADTI_SOLITU	P25083 solanum tub
33	246.5	14.6	298	1 ADT3_HUMAN	P12236 homo sapien

RESULT 1									
UCP4_HUMAN	14.6	382	1	ADT_ORYSA	14.6	382	1	ADT_ORYSA	14.6
ID UCP4_HUMAN	14.5	298	1	ADT3_BOVIN	14.5	298	1	ADT3_BOVIN	14.5
AC O95847	14.5	313	1	ADT_NEUCR	14.5	313	1	ADT_NEUCR	14.5
DT 15-JUL-1999	14.5	308	1	ADT_CHLRE	14.5	308	1	ADT_CHLRE	14.5
DT 15-JUL-1999	14.4	387	1	ADT1_MAIZE	14.4	387	1	ADT1_MAIZE	14.4
DT 15-MAR-2004	14.3	387	1	ADT2_MAIZE	14.3	387	1	ADT2_MAIZE	14.3
DB Mitochondrial uncoupling protein 4 (UCP 4) (UNQ772/PRO1566)	14.1	298	1	ADT1_HUMAN	14.1	298	1	ADT1_HUMAN	14.1
UCP4	14.1	307	1	ADT3_YEAST	14.1	307	1	ADT3_YEAST	14.1
OS Homo sapiens (Human)	14.1	310	1	ODCI_YEAST	14.1	310	1	ODCI_YEAST	14.1
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	14.1	322	1	SFCI_YEAST	14.1	322	1	SFCI_YEAST	14.1
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	13.9	297	1	ADT1_BOVIN	13.9	297	1	ADT1_BOVIN	13.9
OX NCBI_TaxID=9606;	13.9	298	1	ADT1_RAT	13.9	298	1	ADT1_RAT	13.9
RN [1]									
RP SEQUENCE FROM N.A.									
RC TISSUE=Brain;									
RX MEDLINE=99148824; PubMed=10025957;									
RA Mao W., Yu X.X., Zhong A., Li W., Brush J., Sherwood S.W., Adams S.H.,									
RA Pan G.;									
RT "UCP4, a novel brain-specific mitochondrial protein that reduces									
RT membrane potential in mammalian cells."									
RL PEBS Lett. 443:326-330(1999).									
RN [2]									
RP SEQUENCE FROM N.A.									
RX MEDLINE=22887296; PubMed=12975309;									
RA Clark H.F., Gurney A.I., Abaya E., Baker K., Baldwin D., Brush J.,									
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,									
RA Eaton D., Foster J., Grimaldi C., Gu O., Hass P.E., Heldens S.,									
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,									
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,									
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,									
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,									
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,									
RA Godowski P.;									
RT "The secreted protein discovery initiative (SPDI), a large-scale									
RT effort to identify novel human secreted and transmembrane proteins: a									
RT bioinformatics assessment."									
RL Genome Res. 13:2265-2270(2003).									
CC -I- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE									
CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE. THUS									
CC UNCOUPLING OXIDATIVE PHOSPHORYLATION FROM ATP SYNTHESIS. AS A									
CC RESULT, ENERGY IS DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE									
CC IN THERMOREGULATORY HEAT PRODUCTION AND METABOLISM IN BRAIN.									
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial									
CC inner membrane.									
CC -I- TISSUE SPECIFICITY: Found in adult and fetal brain. Present in									
CC most of the brain tissues, with low levels in spinal chord, corpus									
CC callosum and substantia nigra.									
CC -I- SIMILARITY: Belongs to the mitochondrial carrier family.									
CC -I- SIMILARITY: Contains 3 Solcar repeats.									
CC -----									
CC This SWISS-PROT entry is copyright. It is produced through a collaboration									
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -									
CC the European Bioinformatics Institute. There are no restrictions on its									
CC use by non-profit institutions as long as its content is in no way									
CC modified and this statement is not removed. Usage by and for commercial									

ALIGNMENTS

P31691 oryza sativ
P32007 bos taurus
P02723 neurospora
P27080 chlamydomon
P04709 zea mays (m
P12857 zea mays (m
P12235 homo sapien
P18238 saccharomyc
Q03028 saccharomyc
P33303 saccharomyc
P02722 bos taurus
Q05962 rattus norv

entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

```

CC  EMBL; AF110532; AAD16995.1; -
CC  EMBL; AY358711; AAQ89951.1; -
CC  GO; GO:0005739; C:mitochondrion; TAS.
CC  GO; GO:0015302; F:uncoupling protein activity; TAS.
CC  GO; GO:0006091; P:energy pathways; TAS.
CC  InterPro; IPR002030; Mit uncoupling.
CC  InterPro; IPR001993; Mitoch_carrier.
CC  Pfam; PF00153; mito_carr; 3.
CC  PRINTS; PR00784; MTUNCOUPLING.
CC  PROSITE; PS50920; SOLCAR; 3.
CC  Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
CC  TRANSMEM 23 40 1 (POTENTIAL).
CC  TRANSMEM 88 109 2 (POTENTIAL).
CC  TRANSMEM 127 144 3 (POTENTIAL).
CC  TRANSMEM 195 212 4 (POTENTIAL).
CC  TRANSMEM 229 248 5 (POTENTIAL).
CC  TRANSMEM 288 311 6 (POTENTIAL).
CC  REPEAT 21 115 SOLCAR 1.
CC  REPEAT 125 217 SOLCAR 2.
CC  REPEAT 226 317 SOLCAR 3.
CC  DOMAIN 5 8 POLY-GLU.
CC  SEQUENCE 323 AA; 36064 MW; 4C54A56BB10333ED CRC64;
CC  Query Match 100.0%; Score 1690; DB 1; Length 323;
CC  Best Local Similarity 100.0%; Pred. No. 2.2e-131;
CC  Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC  QY 1 MSVPEEERLLPTQRPFRASKFLLSGCAATVAELATFPDLTKRLQMGEEAALRLGD 60
CC  DB 1 MSVPEEERLLPTQRPFRASKFLLSGCAATVAELATFPDLTKRLQMGEEAALRLGD 60
CC
CC  QY 61 GAREAPYRGWVRVLTALGIIIEEGFLKLGQVTPAIRHVYSGRMVYTHLREVWFGKS 120
CC  DB 61 GAREAPYRGWVRVLTALGIIIEEGFLKLGQVTPAIRHVYSGRMVYTHLREVWFGKS 120
CC
CC  QY 121 EDEHYPLWKSIVGGMAGVIGFOFLANPTDLVKVQMGEGKRLGKPLRFRGVHAFPAKI 180
CC  DB 121 EDEHYPLWKSIVGGMAGVIGFOFLANPTDLVKVQMGEGKRLGKPLRFRGVHAFPAKI 180
CC
CC  QY 181 LAEGGIRGLWAGWPNIOALVNNQDLTTVDYTKVHLVLTNPEDNIMTHGLSSLCGL 240
CC  DB 181 LAEGGIRGLWAGWPNIOALVNNQDLTTVDYTKVHLVLTNPEDNIMTHGLSSLCGL 240
CC
CC  QY 241 VASILGTTPADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGGFMSLYKGFPLPSWLRM 300
CC  DB 241 VASILGTTPADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGGFMSLYKGFPLPSWLRM 300
CC
CC  QY 301 TPWSMVFWLTVEKIREMSGVSPF 323
CC  DB 301 TPWSMVFWLTVEKIREMSGVSPF 323
CC
CC  RESULT 2
CC  UCPS5 HUMAN STANDARD; PRT; 325 AA.
CC  AC O95258; Q9HC60; Q9HC61;
CC  DT 30-MAY-2000 (Rel. 39, Created)
CC  DT 30-MAY-2000 (Rel. 39, Last sequence update)
CC  DT 15-MAR-2004 (Rel. 43, Last annotation update)
CC  DE Brain mitochondrial carrier protein-1 (BMCP-1) (Mitochondrial
CC  DE uncoupling protein 5) (UCP 5) (Solute carrier family 25, member 14)
CC  DE (UNQ791/PRO1682).
CC  GN SLC25A14 OR BMCP1 OR UCP5.
CC  OS Homo sapiens (Human).
CC  OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC  OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC  OX NCBI_Taxid=9606;
CC  RN [1]
CC  RP SEQUENCE FROM N.A. (ISOFORM 1).
CC  RL MEDLINE=99069464; PubMed=9852133;

```

```

RA Sanchis D., Fleury C., Chomiki N., Goubern M., Huang Q., Neverova M.,
RA Gregoire F., Eslick J., Rimbault S., Levi-Meyrueis C., Miroux B.,
RA Collins S., Seldin M., Richard D., Warden C., Bouillaud F.,
RA Ricquier D.;
RA "BMCP1, a novel mitochondrial carrier with high expression in the
RA central nervous system of humans and rodents, and respiration
RA uncoupling activity in recombinant yeast.";
RA J. Biol. Chem. 273:34611-34615(1998).
RA [2]
RA SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RA MEDLINE=20387222; PubMed=10928996;
RA Yu X.X., Mao W., Zhong A., Schow P., Brush J., Sherwood S.W.,
RA Adams S.H., Pan G.;
RA "Characterization of novel UCP5/BMCP1 isoforms and differential
RA regulation of UCP4 and UCP5 expression through dietary or temperature
RA manipulation.";
RA FASEB J. 14:1611-1618(2000).
RA [3]
RA SEQUENCE FROM N.A. (ISOFORM 1).
RA MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RA "The secreted protein discovery initiative (SPDI), a large-scale
RA effort to identify novel human secreted and transmembrane proteins: a
RA bioinformatics assessment.";
RA Genome Res. 13:2265-2270(2003).
RA [4]
RA SEQUENCE FROM N.A.
RA Pearce A.;
RA Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RA -I- FUNCTION: Participates to the mitochondrial proton leak measured
CC in brain mitochondria.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -I- ALTERNATIVE PRODUCTS:
CC Name=1; Synonyms=UCP5L;
CC IsoId=O95258-1; Sequence=Displayed;
CC Name=2; Synonyms=UCP5S;
CC IsoId=O95258-2; Sequence=VSP_003272;
CC Name=3; Synonyms=UCP5SI;
CC IsoId=O95258-3; Sequence=VSP_003272, VSP_003273;
CC -I- TISSUE SPECIFICITY: Mainly expressed in brain. Some expression in
CC testis and pituitary.
CC -I- SIMILARITY: Belongs to the mitochondrial carrier family.
CC or send an email to license@isb-sib.ch.
CC -----
CC EMBL; AF078544; AAD04346.1; -
CC EMBL; AF155809; AAG29582.1; -
CC EMBL; AF155810; AAG29583.1; -
CC EMBL; AF155811; AAG29584.1; -
CC EMBL; AY358099; AAO88466.1; -
CC EMBL; AL035423; CAB41251.1; -
CC MIN; 300242; -
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005739; C:mitochondrion; TAS.
CC GO; GO:0005386; F:carrier activity; TAS.

```



```

CC CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
CC CC -!- SIMILARITY: Contains 3 Solcar repeats.
CC CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use by non-profit institutions as long as its content is in no way
CC CC modified and this statement is not removed. Usage by and for commercial
CC CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC CC or send an email to license@sb-sib.ch).
CC CC -----
DR DR EMBL; AF095744; AAD08811.1; -
DR DR EMBL; AF128837; AAD33396.1; -
DR DR InterPro; IPR002067; Mit_carrier.
DR DR InterPro; IPR002030; Mit_uncoupling.
DR DR Pfam; PF00153; mito_carr; 3
DR DR PRINTS; PR00926; MITOCARRIER.
DR DR PRINTS; PR00784; MTUNCOUPLING.
DR DR PROSITE; PS0920; SOLCAR; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 11 32 1 (POTENTIAL).
FT TRANSMEM 74 96 2 (POTENTIAL).
FT TRANSMEM 117 133 3 (POTENTIAL).
FT TRANSMEM 180 196 4 (POTENTIAL).
FT TRANSMEM 214 233 5 (POTENTIAL).
FT TRANSMEM 268 290 6 (POTENTIAL).
FT REPEAT 11 102 SOLCAR 1.
FT REPEAT 111 202 SOLCAR 2.
FT REPEAT 211 296 SOLCAR 3.
FT DOMAIN 275 297 PURINE NUCLEOTIDE BINDING (BY
FT SIMILARITY).
FT CONFLICT 7 8 PE -> SD (IN REF. 2).
FT CONFLICT 13 13 T -> M (IN REF. 2).
FT CONFLICT 17 17 L -> F (IN REF. 2).
FT CONFLICT 49 49 A -> AVQT (IN REF. 2).
FT CONFLICT 150 150 R -> G (IN REF. 2).
SQ SEQUENCE 308 AA; 33772 MW; FDF1F2BC28FDE997 CRC64;

Query Match 28.4%; Score 480.5; DB 1; Length 308;
Best Local Similarity 34.5%; Pred. No. 3.5e-32;
Matches 108; Conservative 64; Mismatches 114; Indels 27; Gaps 6;

QY 20 ASKFLSGCAATVAELATFLDLTKTKLQMGAAALRGDGAESAPYRGVMVRLTGII 79
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
14 AVKLGGAGTAACTADLLTFELDTAKVRLQIQENQAR-----SAQYRGVLGTLTMV 66
QY 80 EEEGFLKMGQVTPAIRVHVYGGRMVTYHLEHREVVGKSEDEHYPLWKSIVGGMAGV 139
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
67 RNEGPRSPYNGLVAGLQRMQSFASIRIGLYDSVKQLYTPKGS-D-HGSITRILAGCTGA 125
QY 140 IQGFLANPTDLVKVQMQE---GKRLEGKPLRPGVHHAFKILAEAGGIRGLWAGVNP 196
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
126 MAVTCQPTDVKVRFOASIHAGRSNR-----KYSGMTDAYRTIAREGVRGLWKGILPN 181
QY 197 IQRAALVNMGLDITVDVHYLVNLTPLDNIHTGLSSICSLGVALISILGTPADVTKSRI 256
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
182 ITRNAIVNCAEMTYDVIKEDYLDYHLLTDNLPCHFVSAGFCATVVASPDVVVKTRY 241
QY 257 MNOPRQKQGLLYKSTDCILQAVQGEPMISYKGLPLPSWLRTWPMVMFWLTYEKIR- 315
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
242 MNSPPGQ-----YQNPDLCKLMKMTQEGTAFYKGTPTPSFLRLGSLGVMVNFVSQELKR 295
QY 316 -----EMSGVSVPF 323
Db |||:||||:
296 ALMKVQMLRESPP 308

RESULT 6
UCP3_HUMAN
ID UCP3_HUMAN STANDARD; PRT; 312 AA.
AC P55916; O60475; Q96HL3;
DT 01-NOV-1997 (Rel. 35, Created)

```

```

DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitochondrial uncoupling protein 3 (UCP 3).
GN UCP3 OR SLC25A9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=97324095; PubMed=9180264;
RA Boss O., Samec S., Paoloni-Giacobino A., Dulloo A., Seydoux J.,
RA Rossier C., Muzzin P., Giacobino J.-P.;
RT "Uncoupling protein-3: a new member of the mitochondrial carrier
RT family with tissue-specific expression.";
RL FEBS Lett. 408:39-42(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS UCP3L AND UCP3S).
RX MEDLINE=97467322; PubMed=9325252;
RA Solanes G., Vidal-Puig A., Grubic D., Flier J.S., Lowell B.B.;
RT "The human uncoupling protein-3 gene. Genomic structure, chromosomal
RT localization, and genetic basis for short and long form
RT transcripts.";
RL J. Biol. Chem. 272:25433-25436(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97450925; PubMed=9305858;
RA Gong D.-W., He Y., Karas M., Reitman M.;
RT "Uncoupling protein-3 is a mediator of thermogenesis regulated by
RT thyroid hormone, beta3-adrenergic agonists, and leptin.";
RL J. Biol. Chem. 272:24129-24132(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=98158426; PubMed=9498661;
RA Uthammer S.A., Dalgaard L.T., Soerensen T.I.A., Tybjaerg-Hansen A.,
RA Erasmund S.M., Andersen T., Clausen J.O., Pedersen O.;
RT "Organisation of the coding exons and mutational screening of the
RT uncoupling protein 3 gene in subjects with juvenile-onset obesity.";
RL Diabetologia 41:241-244(1998).
RN [5]
RP SEQUENCE FROM N.A.
RX PubMed=10958796;
RA Esterbauer H., Oberkofler H., Kremler F., Strosberg A.D., Patech W.;
RT "The uncoupling protein-3 gene is transcribed from tissue-specific
RT promoters in humans but not in rodents.";
RL J. Biol. Chem. 275:36394-36399(2000).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udutin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP VARIANT OBESITY ILE-102.

```

RX MEDLINE=98443224; PubMed=9769326;
 RA Argyropoulos G., Brown A.M., Willi S.M., He Y., Reitman M.,
 RA Gevaso S.M., Spruill I., Garvey W.T.;
 RT "Effects of mutations in the human uncoupling protein 3 gene on the
 RT respiratory quotient and fat oxidation in severe obesity and type 2
 RT diabetes.";
 RL J. Clin. Invest. 102:1345-1351(1998).
 RN (8).
 RP VARIANT OBESITY TRP-70.
 RA Brown A.M., Willi S.M., Argyropoulos G., Garvey W.T.;
 RT "A novel missense mutation, R70W, in the human uncoupling protein 3
 RT gene in a family with type 2 diabetes.";
 RL Hum. Mutat. 13:506-506(1999).
 CC -1- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE
 CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
 CC UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS
 CC DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
 CC OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
 CC ENERGY BALANCE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=UCP3L;
 CC IsoId=P55916-1; Sequence=VSP_003271;
 CC Name=UCP3S;
 CC IsoId=P55916-2; Sequence=VSP_003271;
 CC Name=3;
 CC IsoId=P55916-3; Sequence=VSP_003270;
 CC -1- TISSUE SPECIFICITY: Only in skeletal muscle and heart. Is more
 CC expressed in glycolytic than in oxidative skeletal muscles.
 CC -1- DISEASE: Defects in UCP3 could be involved in severe obesity
 CC (MIM:601665).
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -1- SIMILARITY: Contains 3 Solcar repeats.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U84763; AAC51367.1; -;
 DR EMBL; U82818; AAC51356.1; -;
 DR EMBL; AF001787; AAC51369.1; -;
 DR EMBL; AF011449; AAC51767.1; -;
 DR EMBL; AF012202; AAC51785.1; ALT INIT.
 DR EMBL; AF012197; AAC51785.1; JOINED.
 DR EMBL; AF012198; AAC51785.1; JOINED.
 DR EMBL; AF012199; AAC51785.1; JOINED.
 DR EMBL; AF012200; AAC51785.1; JOINED.
 DR EMBL; AF012201; AAC51785.1; JOINED.
 DR EMBL; AF026958; AAC18822.1; -;
 DR EMBL; AF026956; AAC18822.1; JOINED.
 DR EMBL; AF026957; AAC18822.1; JOINED.
 DR EMBL; AF050113; AAC02284.1; -;
 DR EMBL; BC008392; AAH08392.1; -;
 DR PIR; JC5522; JC5522.
 DR Genew; HGNC:12519; UCP3.
 DR MIM; 602044; -;
 DR MIM; 601665; -;
 DR GO; GO:0005743; C:mitochondrial inner membrane; TAS.
 DR GO; GO:0005739; C:mitochondrion; TAS.
 DR GO; GO:0005215; F:transporter activity; TAS.
 DR GO; GO:0015302; F:uncoupling protein activity; TAS.
 DR GO; GO:0006629; P:lipid metabolism; TAS.
 DR GO; GO:0015992; P:proton transport; TAS.
 DR GO; GO:0007585; P:respiratory gaseous exchange; TAS.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.

DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PRO0926; MITOCARRIER.
 DR PRINTS; PRO0784; MTUNCOUPLING.
 DR PROSITE; PS50920; SOLCAR_3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Alternative splicing; Disease mutation; Diabetes mellitus; Obesity.
 FT TRANSMEM 11 32 1 (POTENTIAL).
 FT TRANSMEM 77 99 2 (POTENTIAL).
 FT TRANSMEM 120 136 3 (POTENTIAL).
 FT TRANSMEM 184 200 4 (POTENTIAL).
 FT TRANSMEM 218 237 5 (POTENTIAL).
 FT TRANSMEM 272 294 6 (POTENTIAL).
 FT REPEAT 11 105 SOLCAR 1.
 FT REPEAT 114 206 SOLCAR 2.
 FT REPEAT 215 300 SOLCAR 3.
 FT DOMAIN 279 301 PURINE NUCLEOTIDE BINDING
 FT VARSPLIC 114 216 (BY SIMILARITY).
 FT VARSPLIC 276 312 Missing (in isoform 3).
 FT VARSPLIC 276 312 Missing (in isoform UCP3S).
 FT VARIAT 70 70 R -> W (in severe obesity with type 2
 FT diabetes).
 FT VARIAT 102 102 /FTId=VAR_004407.
 FT VARIAT 193 194 V -> I (in obesity).
 FT CONFLICT 193 194 /FTId=VAR_004408.
 FT SEQUENCE 312 AA; 34216 MW; D0E04A8DB352B17C CRC64;
 Query Match 28.1%; Score 475.5; DB 1; Length 312;
 Best Local Similarity 35.8%; Pred. No. 9.2e-32;
 Matches 113; Conservative 58; Mismatches 116; Indels 29; Gaps 7;
 QY 20 ASKFLSGCAATVAELATPDLTKRLQWQGE---AALARLGDGARESAFYRGWVRTAL 76
 DB 14 AVKFLGAGTAACFADLVTPDLTAKVRLQIQENQAVQTARL-----VQYRGVLGTIL 66
 QY 77 GIIEEGFLKMQGVTPAIYRHVVYSGGRMVTYHLRVVFGKSEDEHYPLMKSVIGMM 136
 DB 67 TWTRETEGPCSYNGLVAGLQRMSPASIRIGLYDSVKQVYTPKGAD-NSSLTRILAGCT 125
 QY 137 AGVIGOFPLANTDLVKVQWQME---GKRKLEKGLFRGVHFAKILAEGGIRGLWAGW 193
 DB 126 TGAMAVTCAPQTDWVKVRFQASIHGLGPSRDRK---YSGTMDAYRTIAREEGVRGLWKG 182
 QY 194 VPMIOAALVNMGLTLYDTVKHYLVNTPLEDNIMTHGLSSLCGLVASILGTPADVIK 253
 DB 183 LPNIMENAIVNCAEVVYDILKEKLDYHLLTDNFPCHFVSAGFCATVVASPVDVVK 242
 QY 254 SRIMNQPRDKQGRGLLYKSTDCILQAVOGEGPMISLYKGLPSWLKMTWPMVFWLTYEK 313
 DB 243 TRYNSPPGQ-----YFSPFLDKMKNVQAEQGTAFYKGTPTPSFLRLGSLGNNVFMV 296
 QY 314 IR-----EMSGVSPF 323
 DB 297 LKRALMKVQMLRESPP 312
 RESULT 7
 ID UCP3_CANFA STANDARD; PRT; 311 AA.
 AC Q9N219; Q9N219;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Mitochondrial uncoupling protein 3 (UCP 3).
 GN UCP3.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.


```

RA Ishioka K.;
RT "Cloning of canine UCP families.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 14-146 FROM N.A.
RA Thompson G.M., Kelly L.J., Candelore M.R.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE
CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
CC UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS
CC DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
CC OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
CC ENERGY BALANCE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -1- SIMILARITY: Contains 3 Solcar repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: AB022020; BAA90458.1; -
CC EMBL: AF201378; AAF08310.1; -
CC InterPro: IPR002030; Mit_uncoupling.
CC Pfam: PF00153; mito_car; 3.
CC PRINTS: PR00784; MTUNCOUPLING.
CC PROSITE: PS50920; SOLCAR; 3.
CC Mitochondrion; Inner membrane; Repeat: Transmembrane; Transport.
FT TRANSMEM 11 32 1 (POTENTIAL).
FT TRANSMEM 77 99 2 (POTENTIAL).
FT TRANSMEM 120 136 3 (POTENTIAL).
FT TRANSMEM 183 199 4 (POTENTIAL).
FT TRANSMEM 217 236 5 (POTENTIAL).
FT TRANSMEM 271 293 6 (POTENTIAL).
FT REPEAT 11 105 SOLCAR 1.
FT REPEAT 114 205 SOLCAR 2.
FT REPEAT 214 299 SOLCAR 3.
FT DOMAIN 278 300
FT
FT CONFLICT 14 14 A -> G (IN REF. 2).
FT SEQUENCE 311 AA; 34137 MW; A719FB8D66637502 CRC64;

Query Match 28.0%; Score 474; DB 1; Length 311;
Best Local Similarity 34.8%; Pred. No. 1.2e-31;
Matches 109; Conservative 59; Mismatches 121; Indels 24; Gaps 6;

QY 20 ASKFLSGCNAVVAELATPPLDTKTRLQWQGAALRLGDGAREAPVRGWRVLTALGII 79
DB 14 AVKFLGAGTAACPADLLTFPLDTAKVRLQIQGENQATQ-----AARRIQVRGLVLTITWV 69
QY 80 BEEGFLKMGQVTPAIVRYHVHVGSGRMVTVEHLREVVFCKSEDEHYPLMKSVIGGMAGV 139
DB 70 RTGGPSRYNGLVAGLQROMSFASIRIGLYDSVQFYTPKGS-D-HSITRIILAGCTTGA 128
QY 140 IGQFLANPTDLVKVQMQE---GKRKLEGLKPLFRGVHFAFAKILAEAGGIRGLWAGVNP 196
DB 129 MAVSCAQPTDVVKVRQASIHLG---AGSNRKYSGTMDAYRTIAREGVRGLWKGTLPN 184
QY 197 IQRAALVNWGDLTYTIVKHYLVNLTPELDNIMTHGLSSLCGSLVASILGTTPADVTKSRI 256
DB 185 ITRNAIVNCAEMVTDIIEKLDYVHLLTDNFPFCHLISAFAGFCATVWASPDVVKTRY 244
QY 257 MNQPRDKQGRGLLYKSSDCLIOAVQEGPMSLYKGLPSLWRMTWMSVFWLTVEKIR- 315
DB 245 MNSPPGQ-----YCSPLDCMLKXKVTQEGPTAFYKGTFTSFLRLGTNVNVMFVTEQLKR 298
QY 316 -----EMSGVSPF 323

```

```

Db 299 ALMKVQMLRESPF 311
:| |||
UCP3_MOUSE
ID UCP3_MOUSE STANDARD; PRT; 308 AA.
AC P56501; O88293;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitochondrial uncoupling protein 3 (UCP 3).
GN UCP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Sanchis D., Fleury C., Bouillaud F., Ricquier D.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster; TISSUE=Embryo;
RX MEDLINE=98332721; PubMed=9666083;
RA Yoshitomi H., Yamazaki K., Tanaka I.;
RT "Cloning of mouse uncoupling protein 3 cDNA and 5'-flanking region,
RL and its genetic map.";
RL Gene 215:77-84 (1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Skeletal muscle;
RA Grubic D., Zhan C.-Y., Sleiker L.J., Lowell B.B.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skeletal muscle;
RA Son C., Hosoda K., Matsuda J., Nakao K.;
RT "Cloning of mouse UCP3 cDNA.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=99167332; PubMed=10066417;
RA Gong D.W., He Y., Reitman M.L.;
RT "Genomic organization and regulation by dietary fat of the uncoupling
RL protein 3 and 2 genes.";
RL Biochem. Biophys. Res. Commun. 256:27-32 (1999).
RN [6]
RP SEQUENCE OF 84-180 FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Skeletal muscle;
RX MEDLINE=98262957; PubMed=9600108;
RA Shimokawa T., Kato M., Ezaki O., Hashimoto S.;
RT "Transcriptional regulation of muscle-specific genes during myoblast
RL differentiation.";
RL Biochem. Biophys. Res. Commun. 246:287-292 (1998).
RN [7]
RP SEQUENCE OF 162-252 FROM N.A.
RA Yan X., Ramsay T.G.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE
CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
CC UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS
CC DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
CC OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
CC ENERGY BALANCE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -1- SIMILARITY: Contains 3 Solcar repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----

```

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

```

DR EMBL; AF032902; AAB87084.1; -
DR EMBL; AB010742; BAA25697.1; -
DR EMBL; AF030164; AAD01892.1; -
DR EMBL; AB008216; BAA33502.1; -
DR EMBL; AF053352; AAC28328.1; -
DR EMBL; AB013132; BAA31989.1; -
DR EMBL; AF019883; AAB71543.1; -
DR MGD; MGI:109787; Ucp3.
DR GO; GO:0005739; C:mitochondrion; IMP.
DR GO; GO:0015302; F:uncoupling protein activity; IMP.
DR GO; GO:0006631; F:fatty acid metabolism; IMP.
DR GO; GO:0000303; F:response to superoxide; IMP.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS0920; SOLCAR; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 11 32
FT TRANSMEM 74 96
FT TRANSMEM 117 133
FT TRANSMEM 180 196
FT TRANSMEM 214 233
FT TRANSMEM 268 290
FT REPEAT 11 102
FT REPEAT 111 202
FT REPEAT 211 296
FT DOMAIN 275 297
FT CONFLICT 179 179 W -> L (IN REF. 6).
FT SEQUENCE 308 AA; 33910 MW; 12CAD7674DF7D0C3 CRC64;

```

```

Query Match      28.0%; Score 473.5; DB 1; Length 308;
Best Local Similarity 35.0%; Pred. No. 1.3e-31;
Matches 110; Conservative, 63; Mismatches 108; Indels 33; Gaps 8;

Qy 22 KFLSGCAATVAELATPDLTKTRLMQGEAALRLGDCARESAPYRGMVRLTALGIIIE 81
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 16 KFLGAGTAACFADLLTFPLDTAKVRLQIQE-----NPGA-QSVQYRGVLTLTWRT 68
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 82 EGFELKQGVTPALYRHVYVSGRWYIYHLREVFVFGKSEDEHYPLWKSIVGMMAGVIG 141
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 69 EGRSPSYGLVAGLHRQMSFASIRIGLYDSVKQFYTPKQAD-HSSVAIRILAGCTTGAMA 127
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 142 QFLANPTDLVKVQVQ-----MEGRKLEKPLRFGRGVHFAKILAEGLRGGLWAGWVP 195
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 128 VTCAPDTPVVKVRFQAMIRLGTGGERK-----YRGTWDAYRTIARESGVRLWKGWTP 180
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 196 NIQRALVNMGDITTYDTPVHYLVNTPLEDNITWTHGLSLCSGLVASILGTPADVIKSR 255
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 181 NITRNAIVNCAEMVTYDIIEKLESHLFTDNPFCFVSAFGAGFCATVVASPDVVKTR 240
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 256 IMNPRDKQKGLLYKSSDCLTQAVQGGFMSLYGFLPSWLRTPMSPWFWLTYEKTR 315
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 241 YNNAP---LGR---YRSLPHCLMKVQAQEGPTAFYKGFVPSFLRLGAMVNMVFTYEQLK 294
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 316 -----EMSGVSPF 323
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 295 RALMKVQLRESFP 308
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 9
UCP2_HUMAN
ID UCP2_HUMAN
AC P55851;

```

```

DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitochondrial uncoupling protein 2 (UCP 2) (UCPH).
GN UCP2 OR SLC25A8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=97324095; PubMed=9180264;
RA Boes O., Samec S., Paoloni-Giacobino A., Dulloo A., Seydoux J.,
RA Rossier C., Muzzin P., Giacobino J.-P.;
RT "Uncoupling protein-3: a new member of the mitochondrial carrier
RT family with tissue-specific expression.";
RL FEBS Lett. 408:39-42(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung, and Skeletal muscle;
RX MEDLINE=97207646; PubMed=9054939;
RA Fleury C., Neverova M., Collins S., Raimbault S., Champigny O.,
RA Levi-Meyrueis C., Bouillaud F., Seldin M.F., Surwit R.S.,
RA Ricquier D., Warden C.H.;
RT "Uncoupling protein-2: a novel gene linked to obesity and
RT hyperinsulinemia.";
RL Nat. Genet. 15:269-272(1997).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT VAL-55.
RC TISSUE=Spleen;
RX MEDLINE=97278985; PubMed=9133562;
RA Gimeno R.E., Dembeki M., Weng X., Deng N., Shyjan A.W.,
RA Gimeno C.J., Iris F., Ellis S.J., Woolf E.A., Tartaglia L.A.;
RT "Cloning and characterization of an uncoupling protein homolog: a
RT potential molecular mediator of human thermogenesis.";
RL Diabetes 46:900-906(1997).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT VAL-55.
RC Klanenmark M., Orzho M., Groop L.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=98227655; PubMed=9568704;
RA Argyropoulos G., Brown A.M., Peterson R., Likes C.E., Watson D.K.,
RA Garvey W.T.;
RT "Structure and organization of the human uncoupling protein 2 gene and
RT identification of a common biallelic variant in Caucasian and African-
RT American subjects.";
RL Diabetes 47:685-687(1998).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=99185293; PubMed=10082652;
RA Pecqueur C., Cassard-Doulcier A.M., Raimbault S., Miroux B.,
RA Fleury C., Gelly C., Bouillaud F., Ricquier D.;
RT "Functional organization of the human uncoupling protein-2 gene, and
RT juxtaposition to the uncoupling protein-3 gene.";
RL Biochem. Biophys. Res. Commun. 255:40-46(1999).
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=B-Cell;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

```


predominant expression in the heart, lung and spleen.
 -!- SIMILARITY: Belongs to the mitochondrial carrier family.
 -!- SIMILARITY: Contains 3 Solcar repeats.

 This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

 EMBL; AF039033; AAC98733.1; -
 EMBL; AB006613; BAA23383.1; -
 EMBL; AB010743; BAA25698.1; -
 EMBL; AB005143; BAA28832.1; -
 InterPro; IPR002030; Mit_uncoupling.
 InterPro; IPR001993; Mitoch_carrier.
 Pfam; PF00153; mito_car; 3.
 PRINTS; PR00784; MTUNCOUPLING.
 PROSITE; PS0920; SOLCAR; 3.

Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 TRANSMEM 11 32 1 (POTENTIAL).
 TRANSMEM 78 100 2 (POTENTIAL).
 TRANSMEM 120 136 3 (POTENTIAL).
 TRANSMEM 181 197 4 (POTENTIAL).
 TRANSMEM 215 234 5 (POTENTIAL).
 TRANSMEM 269 291 6 (POTENTIAL).
 REPEAT 11 106 SOLCAR 1.
 REPEAT 114 203 SOLCAR 2.
 REPEAT 212 297 SOLCAR 3.
 DOMAIN 276 298

CONFLICT 9 9 V -> L (IN REF. 4).
 CONFLICT 268 268 A -> T (IN REF. 3).
 SEQUENCE 309 AA; 33376 MW; 3297935CF997AA0E CRC64;

Query Match 28.0%; Score 473.5; DB 1; Length 309;
 Best Local Similarity 35.0%; Pred. No. 1.3e-31;
 Matches 105; Conservative 65; Mismatches 113; Indels 17; Gaps 6;

18 PRAS-KFTLSCAATVAELATFPLDLTKRLQMGEEA-ALARGDGAAPRGWRTA 75
 11 PTATVKFLGAGTACIADLTFFLDLTAKRLQIQGE-----TAASAQYRGVLGTI 66
 76 LGITEEGFLKMGQVTPAIYRHVYSGRMVTVYHLREVVGKSEDEHYPLWKSIVGGM 135
 67 LTMVTEGPRSLYGLVAGLQRMSPASVRIGLYDSVKQ---FYTKGSEHAGIGSRLLAGS 124
 136 MAGVIGQFLANPTDLVKVQMGEGKRLKGLKPLFRGVHFAKILAEGGIRGLWAGWVP 195
 125 TTGALAVAVAQPTDVVKVRFQAQAR---AGGRRYQSTVEAYKTIAREEGIRGLWKGTS 181
 196 NIQRAALVNMGDLTYYDTVKHYLVNLTPLDNTMTHGLSLCSGLVASILGTADVIKSR 255
 182 NVARNAINVNCETLVYDLIKDALLKANLMTDDLPCHFTSAFGAGCTCTVIASPDVVVKTR 241
 256 IMNQPRDKQGRGLLYKSTDCILQAVQGEFMSLYKGLFPLSWLRMTFWSWFWLTVEKIR 315
 242 YMNSALGQ-----YHSAGHCALTMRLKEGPRAFYKGFMPSEFLRLGSMVNVVETVEQLK 295

RESULT 11
 UCP2_CANFA
 ID UCP2_CANFA STANDARD; PRT; 309 AA.
 AC Q9N2J1; Q9T7T0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Mitochondrial uncoupling protein 2 (UCP 2).
 GN UCP2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI TaxID=9615;
 [1]
 RN SEQUENCE FROM N.A.
 RA Ishioka K.;
 RT "Cloning of canine UCP families";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE OF 4-197 FROM N.A.
 RA Thompson G.M., Kelly L.J., Candellone M.R.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: UCP are mitochondrial transporter proteins that create proton leaks across the inner mitochondrial membrane, thus uncoupling oxidative phosphorylation from ATP synthesis. As a result, energy is dissipated in the form of heat (By similarity).
 CC -!- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -!- SIMILARITY: Contains 3 Solcar repeats.

 This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

 EMBL; AB020887; BAA90457.1; -
 EMBL; AF201377; AAF08309.1; -
 InterPro; IPR002030; Mit_uncoupling.
 InterPro; IPR001993; Mitoch_carrier.
 Pfam; PF00153; mito_car; 3.
 PRINTS; PR00784; MTUNCOUPLING.
 PROSITE; PS0920; SOLCAR; 3.

Mitochondrion; Transmembrane; Transport; Repeat.
 TRANSMEM 11 32 1 (POTENTIAL).
 TRANSMEM 78 100 2 (POTENTIAL).
 TRANSMEM 120 136 3 (POTENTIAL).
 TRANSMEM 181 197 4 (POTENTIAL).
 TRANSMEM 215 234 5 (POTENTIAL).
 TRANSMEM 269 291 6 (POTENTIAL).
 REPEAT 11 106 SOLCAR 1.
 REPEAT 114 203 SOLCAR 2.
 REPEAT 212 297 SOLCAR 3.
 DOMAIN 276 298

CONFLICT 64 64 PURINE NUCLEOTIDE BINDING (BY
 CONFLICT 309 AA; 33270 MW; D9860F0EA8B870BF CRC64;
 SEQUENCE 309 AA; 33270 MW; D9860F0EA8B870BF CRC64;

Query Match 28.0%; Score 472.5; DB 1; Length 309;
 Best Local Similarity 35.0%; Pred. No. 1.6e-31;
 Matches 105; Conservative 63; Mismatches 115; Indels 17; Gaps 6;

18 PRAS-KFTLSCAATVAELATFPLDLTKRLQMGEEAALARGD-GARESAPYRGWRTA 75
 11 PTATVKFLGAGTACIADLTFFLDLTAKRLQIQGE---RQGPVRAAASQYRGVLCTI 66
 76 LGITEEGFLKMGQVTPAIYRHVYSGRMVTVYHLREVVGKSEDEHYPLWKSIVGGM 135
 67 LTMVTEGPRSLYGLVAGLQRMSPASVRIGLYDSVKQ---FYTKGSEHAGIGSRLLAGS 124
 136 MAGVIGQFLANPTDLVKVQMGEGKRLKGLKPLFRGVHFAKILAEGGIRGLWAGWVP 195
 125 TTGALAVAVAQPTDVVKVRFQAQAR---AGGRRYQSTVDYKTIAREEGIRGLWKGTS 181
 196 NIQRAALVNMGDLTYYDTVKHYLVNLTPLDNTMTHGLSLCSGLVASILGTADVIKSR 255
 182 NVARNAINVNCETLVYDLIKDALLKANLMTDDLPCHFTSAFGAGCTCTVIASPDVVVKTR 241
 256 IMNQPRDKQGRGLLYKSTDCILQAVQGEFMSLYKGLFPLSWLRMTFWSWFWLTVEKIR 315

242 YMSALGQ-----YSSAGHCALTMLOKEGPRAPYKGFMPFSLRLGSGWNVVMTVYBQLK 295

Db

RESULT 12

UCP2 MOUSE

ID UCP2_MOUSE STANDARD; PRT; 309 AA.

AC P70406; 088285;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Mitochondrial uncoupling protein 2 (UCP 2) (UCPH).

GN UCP2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c; TISSUE=Muscle;

RA Raimbault S., Bouillaud F., Ricquier D.;

RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RX MEDLINE=97278985; PubMed=9133562;

RA Gimeno R.E., Dembski M., Weng X., Deng N., Shyjan A.W.,

RA Gimeno C.J., Iris F., Ellis S.J., Woolf E.A., Tartaglia L.A.;

RT "Cloning and characterization of an uncoupling protein homolog: a

RT potential molecular mediator of human thermogenesis.";

RL Diabetes 46:900-906(1997).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6 X CBA;

RX MEDLINE=98374026; PubMed=9710252;

RA Yamada M., Hashida T., Shibusawa N., Iwasaki T., Murakami M.,

RA Monden T., Satoh T., Mori M.;

RT "Genomic organization and promoter function of the mouse uncoupling

RT protein 2 (UCP2) gene.";

RL FEBS Lett. 432:65-69(1998).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Colon, and Mammary gland;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: UCP are mitochondrial transporter proteins that create

CC proton leaks across the inner mitochondrial membrane, thus

CC uncoupling oxidative phosphorylation from ATP synthesis. As a

CC result, energy is dissipated in the form of heat (By similarity).

CC -!- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial

CC inner membrane.

CC -!- TISSUE SPECIFICITY: HIGHEST IN WHITE ADIPOSE TISSUE BUT ALSO

CC DETECTED IN BROWN ADIPOSE TISSUE, HEART, AND KIDNEY. 4-6 TIMES

CC HIGHER LEVELS ARE DETECTED IN OB/OB AND DB/DB MICE.

CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.

CC -!- SIMILARITY: Contains 3 Solcar repeats.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.ebi.ac.uk/ebis-sib.ch/>).

CC or send an email to license@sib-sib.ch.

CC -----

DR EMBL; U99135; AAB17666.1; -

DR EMBL; U94593; AAB53092.1; -

DR EMBL; AB012159; BAA32532.1; -

DR EMBL; BC012697; AAH12697.1; -

DR EMBL; BC012967; AAH12967.1; -

DR MGD; MGI:109354; Ucp2.

DR InterPro; IPR002030; Mit. uncoupling.

DR InterPro; IPR001993; Mitoch. carrier.

DR Pfam; PF00153; mito carr; 3.

DR PRINTS; PR00784; MTUNCOUPLING.

DR PROSITE; PS50920; SOLCAR; 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.

FT TRANSMEM 11 32 1 (POTENTIAL).

FT TRANSMEM 78 100 2 (POTENTIAL).

FT TRANSMEM 120 136 3 (POTENTIAL).

FT TRANSMEM 181 197 4 (POTENTIAL).

FT TRANSMEM 215 234 5 (POTENTIAL).

FT TRANSMEM 269 291 6 (POTENTIAL).

FT REPEAT 11 106 SOLCAR 1.

FT REPEAT 114 203 SOLCAR 2.

FT REPEAT 212 297 SOLCAR 3.

FT DOMAIN 276 298

FT CONFLICT 285 285 V -> I (IN REF. 3).

FT SIMILARITY.

SQ SEQUENCE 309 AA; 33373 MW; 329794EEA99810E5 CRC64;

Query Match 28.0%; Score 472.5; DB 1; Length 309;

Best Local Similarity 34.1%; Pred. No. 1.6e-31;

Matches 107; Conservative 66; Mismatches 118; Indels 23; Gaps 7;

QY 18 PRAS-KFLSLGCAATVAELATPPLDITKRLQWQGEA-ALARLGDGAREAPYRGWVRTA 75

DB 11 PTATVKFLGAGTAACIADLTITPDLDTAKVRLQIQGESQGLVR---TAASAQYRGVLGTI 66

QY 76 LGIIEEGELKMQGVTPALYRHVVYSGRWVYEHLEHREVVFCKSEDEHYPLKSVIGGM 135

DB 67 LTMVTRTEGPRSLYNGLVAGLQRMQSFASVRIGLYDSVKQ--FYTKGSEHAGIGSRLLAGS 124

QY 136 MAGVIGQFLANPTDLVKVQMQMEGKRKLEKPLRFRGVHFAKILAEGGIRGLWAGWVP 195

DB 125 TTGALAVAVAQPTDVVKVRFQAQAR---AGGRRYQSTVEAYKTIAREEGIRGLWKTSP 181

QY 196 NTQRAALVNMGLDITVYDVTKVHLVNLPTLEDNIMTHGLSLCSGLVASILGTTPADVIKSR 255

DB 182 NVARNAINVCAELVTYDLIKTLKANLMTDDLPCHTSAFGAGFCTTIVIASPVDVVKTR 241

QY 256 INMQPRDKOGRGLLYKSSDCLIAQVQGGFMSLYKGLFPLPSWLMPTPWSVFWLTVEKIR 315

DB 242 YMSALGQ-----YHSAGHCALTMRLKEGPRAPYKGFMPFSLRLGSGWNVVMTVYBQLK 295

QY 316 E-----MSGVSPF 323

DB 296 RALMAAYQREAPF 309

RESULT 13

UCP2_PIG

ID UCP2_PIG STANDARD; PRT; 309 AA.

AC Q97562; Q9GK29;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2004, 03:35:42 ; Search time 86 Seconds
(without alignments)

1185.028 Million cell updates/sec

Title: US-09-397-342C-1

Perfect score: 1690

Sequence: 1 MSVPSEERLLPLTORPRA.....SMVFMLTYKIREMSGVSPF 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organella:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1621	95.9	322	11 Q9D6D0	Q9d6d0 mus musculus
2	1603.5	94.9	322	11 Q9EPH7	Q9eph7 rattus norv
3	1480.5	87.6	344	11 Q9EPH6	Q9eph6 rattus norv
4	1480.5	87.6	365	11 Q9EPH5	Q9eph5 rattus norv
5	1319	78.0	283	11 Q9CX10	Q9cx10 mus musculus
6	1221	72.2	245	4 Q8N518	Q8n518 homo sapien
7	1192.5	70.6	315	13 Q773F5	Q773f5 brachydanio
8	933	55.2	340	5 Q9VX14	Q9vx14 drosophila
9	793.5	47.0	324	5 Q01883	Q01883 caenorhabdi
10	726.5	43.0	337	5 Q9VNMK0	Q9vnmk0 drosophila
11	667.5	39.5	305	10 Q9XI74	Q9xi74 arabidopsis
12	632	37.4	314	10 Q7XTC5	Q7xtc5 oryza sativ
13	570	33.7	291	11 Q9CR58	Q9cr58 mus musculus
14	561	33.2	210	10 Q8S4C4	Q8s4c4 zea mays (m
15	556	32.9	335	5 Q9VNMK1	Q9vnmk1 drosophila
16	552.5	32.7	353	11 Q8CJ24	Q8cj24 mus musculus

ALIGNMENTS

RESULT 1

ID	Q9D6D0	PRELIMINARY;	PRT;	322 AA.
AC	Q9D6D0;			
DT	01-JUN-2001 (TrEMBLrel. 17, Created)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	3632410G24RIK protein (Uncoupling protein UCP-4) (Uncoupling protein 4).			
DE	4).			
GN	3632410G24RIK OR UCP4.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Brain;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann M., Gaasterland T., Giesi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,			
RA	Hayashizaki Y.,			
RT	"Functional annotation of a full-length mouse cDNA collection."			
RL	Nature 409:685-690(2001).			
RN	[2]			

Q8cj23 mus musculus
Q9jnh0 rattus norv
Q9ep88 rattus norv
Q81845 arabidopsis
Q81nzi helicodicer
Q8hx3 macaca fasc
Q24391 solanum tub
Q9avg1 oryza sativ
Q65623 arabidopsis
Q8sa58 lycopersico
Q9zng1 arabidopsis
Q7zv6 brachydanio
Q9vnm8 drosophila
Q9avg2 oryza sativ
Q7tny4 dicrotonyx
Q7zrp4 brachydanio
Q90x50 meleagris g
Q7yrf3 antechinus
Q9r246 mus musculus
Q9er17 phodopus su
Q98t90 eupetomena
Q7zxn1 xenopus lae
Q9cdt7 gallus gall
Q9fxg6 tritium ae
Q8cbu0 mus musculus
Q8aym4 gallus gall
Q9fxg5 tritium ae
Q9er16 phodopus su

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;
 RA Hitomi Y., Moriya S., Matsushita K., Tanaka H.;
 RT "Molecular cloning of mouse UCP4 cDNA."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AK014394; BAB29320.1; -;
 DR EMBL; AK043831; BAC31670.1; -;
 DR EMBL; AB106930; BAC66453.1; -;
 DR MGD; MGI:1921261; 3632410G24Rik.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0006839; P:mitochondrial transport; IEA.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS002030; Mit uncoupling.
 DR InterPro; IPR002030; Mit uncoupling.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 2.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 322 AA; 35798 MW; 9C8A413DD28E1B8A CRC64;
 Query Match 95.9%; Score 1621; DB 11; Length 322;
 Best Local Similarity 96.2%; Pred. No. 5.8e-130;
 Matches 306; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 QY 6 EEEELLPQWRPRASKFLLSGCAATVAELATPFLDLTKRLQMGGAALRLGDGARES 65
 DB 5 EEEKLLPQWRPRTSFLLSGCAATVAELATPFLDLTKRLQMGGAALRLGDGAVDS 64
 QY 66 APYRGWRTALGIIEEGFGLKMGVTPAIYRHVVYSGGRMTVEHLREVVFGKSEDEHY 125
 DB 65 APYRGWRTALGIIEEGFGLKMGVTPAIYRHVVYSGGRMTVEHLREVVFGKSEDKHY 124
 QY 126 PLKWSVIGGMWAGVIGQFLANPTDLVKVQMGEGKRLGKPLRFRGVHAFKILAEAG 185
 DB 125 PLKWSVIGGMWAGVIGQFLANPTDLVKVQMGEGKRLGKPLRFRGVHAFKILAEAG 184
 QY 186 IRLGAGWPNIQRAALVNNMGDLTYYDVTKHYLVNLTPLDNTMTHGLSLCSGLVASIL 245
 DB 185 IRLGAGWPNIQRAALVNNMGDLTYYDVTKHYLVNLTPLDNTMTHGLSLCSGLVASIL 244
 QY 246 GTPADVIKSRIMQPRDKQGRGLLYKSSDCLIQAVQGEFGFMSLYKGFPSWLRMTPSM 305
 DB 245 GTPADVIKSRIMQPRDKQGRGLLYKSSADCLIQAVQGEFGFMSLYKGFPSWLRMTPSM 304
 QY 306 VFVLTVEKIREMSGVSPP 323
 DB 305 VFVLTVEKIREMSGVSPP 322
 RESULT 2
 Q9EPH7 PRELIMINARY; PRT; 322 AA.
 ID Q9EPH7
 AC Q9EPH7
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DE 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Uncoupling protein UCP-4, isoform a.
 GN UCP-4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 [1]
 NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague Dawley; TISSUE=Brain;
 RA Alberati-Giani D., Gatti S., Rial E., Danel F., Hauser N.,
 RA Bubendorf C., Bartfai T.;
 RT "Three different isoforms of UCP-4 are expressed in rat preoptic
 anterior hypothalamus."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AJ300162; CAC20898.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0006839; P:mitochondrial transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 2.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 322 AA; 35837 MW; 454580DCA80A9F90 CRC64;
 Query Match 94.9%; Score 1603.5; DB 11; Length 322;
 Best Local Similarity 94.1%; Pred. No. 1.8e-128;
 Matches 304; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
 QY 1 MSVPEEEERLLPQWRPRASKFLLSGCAATVAELATPFLDLTKRLQMGGAALRLGD 60
 DB 1 MPPEEES-LQPLTQWRPRTSFLLSGCAATVAELATPFLDLTKRLQMGGAALAKLGD 59
 QY 61 GARESAPYRGWRTALGIIEEGFGLKMGVTPAIYRHVVYSGGRMTVEHLREVVFGKS 120
 DB 60 GAMESAPYRGWRTALGIIEEGFGLKMGVTPAIYRHVVYSGGRMTVEHLREVVFGKS 119
 QY 121 EDEHPLKWSVIGGMWAGVIGQFLANPTDLVKVQMGEGKRLGKPLRFRGVHAFKILAE 180
 DB 120 EDEHPLKWSVIGGMWAGVIGQFLANPTDLVKVQMGEGKRLGKPLRFRGVHAFKILAE 179
 QY 181 LAEGGIRGLWAGWPNIQRAALVNNMGDLTYYDVTKHYLVNLTPLDNTMTHGLSLCSGL 240
 DB 180 LAEGGIRGLWAGWPNIQRAALVNNMGDLTYYDVTKHYLVNLTPLDNTMTHGLSLCSGL 239
 QY 241 VASILGTPADVIKSRIMQPRDKQGRGLLYKSSDCLIQAVQGEFGFMSLYKGFPSWLRM 300
 DB 240 VASILGTPADVIKSRIMQPRDKQGRGLLYKSSDCLIQAVQGEFGFMSLYKGFPSWLRM 299
 QY 301 TPWSMVFWLTVEKIREMSGVSPP 323
 DB 300 TPWSMVFWLTVEKIREMSGVSPP 322
 RESULT 3
 Q9EPH6 PRELIMINARY; PRT; 344 AA.
 ID Q9EPH6
 AC Q9EPH6
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Uncoupling protein UCP-4, isoform b.
 GN UCP-4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 [1]
 NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague Dawley; TISSUE=Brain;
 RA Alberati-Giani D., Gatti S., Rial E., Danel F., Hauser N.,
 RA Bubendorf C., Bartfai T.;

RT "Three different isoforms of UCP-4 are expressed in rat preoptic
 RT anterior hypothalamus.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

DR EMBL; AJ300163; CAC20899.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.

DR GO; GO:0005739; C:mitochondrion; IEA.

DR GO; GO:0005488; P:binding; IEA.

DR GO; GO:0006839; P:mitochondrial transport; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR001993; Mitoch_carrier.

DR InterPro; IPR002030; Mit uncoupling.

DR Pfam; PF00153; mito carr; 3.

DR PRINTS; PR00784; MTUNCOUPLING.

DR PROSITE; PS00215; MITOCH_CARRIER; 2.

KW Membrane; Transmembrane; Transport.

SQ SEQUENCE 344 AA; 38114 MW; 600ACBSF366BADAA CRC64;

Query Match 87.6%; Score 1480.5; DB 11; Length 344;

Best Local Similarity 94.3%; Pred. No. 6.2e-118;

Matches 283; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 MSVPSEERLLPTQWRPRASKFLLSGCAATVAELATFPDLTKTRLQMOGEAALAKLGD 60

DB 1 MPFPEES-LQPLTQRWPRTSKFLSGCAATVAELATFPDLTKTRLQMOGEAALAKLGD 59

QY 61 GARESPYRGWVTALGIIEEGFLKMQGVTPIYRHVVYSGRMVYEHLEVVFGKS 120

DB 60 GAMESAPYRGWMTALGIQVEEGFLKMQGVTPIYRHVVYSGRMVYEHLEVVFGKS 119

QY 121 EDEHYPLWKSIVIGMWAGVIGQFLANPTDLVKVQMQMEGKRLGKPLRFRGVHHAFAKI 180

DB 120 EDEHYPLWKSIVIGMWAGVIGQFLANPTDLVKVQMQMEGKRLGKPLRFRGVHHAFAKI 179

QY 181 LAEGGIRGLWAGWPNIQRAALVNMGLTFTYDVTKHYLVNLTPLEDNIMTHGLSSLCGSL 240

DB 180 LAEGGIRGLWAGWPNIQRAALVNMGLTFTYDVTKHYLVNLTPLEDNIMTHGLSSLCGSL 239

QY 241 VASILGTADVIKSRIMNQPRDKQGRGLLYKSTDCLIQAVQEGFMSLYKGLPWSLRM 300

DB 240 VASILGTADVIKSRIMNQPRDKQGRGLLYKSTDCVIQAVQEGFMSLYKGLPWSLRM 299

RESULT 4
 Q9EPH5

ID Q9EPH5 PRELIMINARY; PRT; 365 AA.

AC Q9EPH5;

DT 01-MAR-2001 (T-EMBLrel. 16, Created)

DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Uncoupling protein UCP-4, isoform C.

GN UCP-4.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague Dawley; TISSUE=Brain;

RA Alberati-Giani D., Gatti S., Rial E., Danel F., Hauser N.,

RA Bubendorff C., Bartfai T.

RT "Three different isoforms of UCP-4 are expressed in rat preoptic

RT hypothalamus.";

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

DR EMBL; AJ300164; CAC20900.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.

DR GO; GO:0005739; C:mitochondrion; IEA.

DR GO; GO:0005488; P:binding; IEA.

DR GO; GO:0006839; P:mitochondrial transport; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002030; Mit uncoupling.

DR Pfam; PF00153; mito carr; 3.

DR PRINTS; PR00784; MTUNCOUPLING.

DR PROSITE; PS00215; MITOCH_CARRIER; 2.

KW Membrane; Transmembrane; Transport.

SQ SEQUENCE 365 AA; 41144 MW; 477B389BBE1F7525 CRC64;

Query Match 87.6%; Score 1480.5; DB 11; Length 365;

Best Local Similarity 94.3%; Pred. No. 6.7e-118;

Matches 283; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 MSVPSEERLLPTQWRPRASKFLLSGCAATVAELATFPDLTKTRLQMOGEAALAKLGD 60

DB 1 MPFPEES-LQPLTQRWPRTSKFLSGCAATVAELATFPDLTKTRLQMOGEAALAKLGD 59

QY 61 GARESPYRGWVTALGIIEEGFLKMQGVTPIYRHVVYSGRMVYEHLEVVFGKS 120

DB 60 GAMESAPYRGWMTALGIQVEEGFLKMQGVTPIYRHVVYSGRMVYEHLEVVFGKS 119

QY 121 EDEHYPLWKSIVIGMWAGVIGQFLANPTDLVKVQMQMEGKRLGKPLRFRGVHHAFAKI 180

DB 120 EDEHYPLWKSIVIGMWAGVIGQFLANPTDLVKVQMQMEGKRLGKPLRFRGVHHAFAKI 179

QY 181 LAEGGIRGLWAGWPNIQRAALVNMGLTFTYDVTKHYLVNLTPLEDNIMTHGLSSLCGSL 240

DB 180 LAEGGIRGLWAGWPNIQRAALVNMGLTFTYDVTKHYLVNLTPLEDNIMTHGLSSLCGSL 239

QY 241 VASILGTADVIKSRIMNQPRDKQGRGLLYKSTDCLIQAVQEGFMSLYKGLPWSLRM 300

DB 240 VASILGTADVIKSRIMNQPRDKQGRGLLYKSTDCVIQAVQEGFMSLYKGLPWSLRM 299

RESULT 5
 Q9CX10

ID Q9CX10 PRELIMINARY; PRT; 283 AA.

AC Q9CX10;

DT 01-JUN-2001 (T-EMBLrel. 17, Created)

DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE D530043E16RIK protein.

GN 3632410G24RIK OR D530043E16RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Stomach;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Harai A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojbori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Maehima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtauki S.,

RA Hayashizaki Y.

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

DR EMBL; AK021314; BAB32369.1; -.

DR MGD; MGI:1921261; 3632410G24RIK.

```

DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005743; C: mitochondrial inner membrane; IEA.
DR GO: GO:0005739; C: mitochondrion; IEA.
DR GO: GO:0005488; P: binding; IEA.
DR GO: GO:0006839; P: mitochondrial transport; IEA.
DR GO: GO:0006810; P: transport; IEA.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 283 AA; 31122 MW; 8645127817A51864 CRC64;

Query Match 78.0%; Score 1319; DB 11; Length 283;
Best Local Similarity 95.1%; Pred. No. 2.9e-104;
Matches 250; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Qy 6 EEEELLLPTQWRPRASKFLSLGGCAATVAELATFPDLTKTRLMQGEAALRLGDGARES 65
Db 5 EEEKLLPTQWRPTSKFLSLGGCAATVAELATFPDLTKTRLMQGEAALRLGDGAVDS 64

Qy 66 APYRGWVRTALGIIEEGFLKLWGQVTPAIYRHVVYSGGRMVTYEHRLREVVFVFGKSEDEHY 125
Db 65 APYRGWVRTALGIIVQEGFLKLWGQVTPAIYRHVVYSGGRMVTYEHRLREVVFVFGKSEDKHY 124

Qy 126 PLWKSIVGGMWAGVIGQFLANPTDLVKVQMGEGRKLEKGLRFRGVHHAFAKILAEQG 185
Db 125 PLWKSIVGGMWAGVIGQFLANPTDLVKVQMGEGRKLEKGLRFRGVHHAFAKILAEQG 184

Qy 186 IRLGLWAGWPNIQRAALVNMGLTDTYDVKHVYLVNTPLEDNIMTHGLSLCSGLVASIL 245
Db 185 IRLGLWAGWPNIQRAALVNMGLTDTYDVKHVYLVNTPLEDNIMTHGLSLCSGLVASIL 244

Qy 246 GTPADVIKSRIMNPRDKQGRGL 268
Db 245 GTPADVIKSRIMNPRDKQGRSV 267

RESULT 6
Q8N518 ID Q8N518 PRELIMINARY; PRT; 245 AA.
AC Q8N518;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to uncoupling protein 4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC033091; AAH33091.1;
DR GO: GO:0005743; C: mitochondrial inner membrane; IEA.
DR GO: GO:0005488; P: binding; IEA.
DR GO: GO:0006810; P: transport; IEA.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 2.
DR PROSITE: PS00215; MITOCH_CARRIER; 1.
SQ SEQUENCE 245 AA; 27237 MW; 4D1C41017B67DA68 CRC64;

Query Match 72.2%; Score 1221; DB 4; Length 245;
Best Local Similarity 99.6%; Pred. No. 5.4e-96;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSVPEEERLLPTQWRPRASKFLSLGGCAATVAELATFPDLTKTRLMQGEAALRLGD 60
Db 1 MSVPEEERLLPTQWRPRASKFLSLGGCAATVAELATFPDLTKTRLMQGEAALRLGD 60

Qy 61 GARESAPYRGWVRTALGIIEEGFLKLWGQVTPAIYRHVVYSGGRMVTYEHRLREVVFVFGKS 120
Db 61 GARESAPYRGWVRTALGIIEEGFLKLWGQVTPAIYRHVVYSGGRMVTYEHRLREVVFVFGKS 120

Qy 121 EDEHYPLWKSIVGGMWAGVIGQFLANPTDLVKVQMGEGRKLEKGLRFRGVHHAFAK 180
Db 121 EDEHYPLWKSIVGGMWAGVIGQFLANPTDLVKVQMGEGRKLEKGLRFRGVHHAFAK 180

Qy 181 LAEGGIRGLWAGWPNIQRAALVNMGLTDTYDVKHVYLVNTPLEDNIMTHGLSS 235
Db 181 LAEGGIRGLWAGWPNIQRAALVNMGLTDTYDVKHVYLVNTPLEDNIMTHGLSS 235

RESULT 7
Q7T3F5 ID Q7T3F5 PRELIMINARY; PRT; 315 AA.
AC Q7T3F5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shemmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zebberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Uedin T.B.; Toshiyuki S.; Carninci P.; Prange C.;
RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullany S.J.;
RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahy J.; Helton E.; Kettaman M.; Madan A.; Rodrigues S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;
RA Krzywinski M.I.; Skalska U.; Smalhus D.E.; Schnerch A.; Schein J.E.;
RA Jones S.J.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC053139; AAH53139.1;
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 315 AA; 34978 MW; 50B5BEF85386524E CRC64;

Query Match 70.6%; Score 1192.5; DB 13; Length 315;
Best Local Similarity 69.5%; Pred. No. 2e-93;
Matches 214; Conservative 46; Mismatches 47; Indels 1; Gaps 1;

Qy 16 RWRPRASKFLSLGGCAATVAELATFPDLTKTRLMQGEAALRLGDGARESAPYRGWVRTA 75
Db 9 RWRPRVSKFTLSACAAVAELVTFPLDLTKTRLMQGEAALRLGDGARESAPYRGWVRTA 67

Qy 76 LGIIEEGFLKLWGQVTPAIYRHVVYSGGRMVTYEHRLREVVFVFGKSEDEHYPLWKSIVG 135
Db 68 AGIVREEGFLKLWGQVTPAIYRHVVYSGGRMVTYEHRLREVVFVFGKSEDEHYPLWKSIVG 127

Qy 136 MAGVIGQFLANPTDLVKVQMGEGRKLEKGLRFRGVHHAFAKILAEGGIRGLWAGWPN 195
Db 136 MAGVIGQFLANPTDLVKVQMGEGRKLEKGLRFRGVHHAFAKILAEGGIRGLWAGWPN 195

```

```

Db 128 ISGALGOFIASPTDLVKVQVQMEGRRLKGGPRVRGVYHFTKIVAQGGIRGLWAGWVP 187
Qy 196 NIORAALVNMGDLTTTDTVKHYLVNTPLENDIMTHGLSLCGLVASILGTADVIKSR 255
Db 188 NVORAAVLNGLMTYDTVKHFLRNTSIPDNSICHLSSICGLVNAATGTADVVKTR 247
Qy 256 IMNQPRDKQGRGLLYKSSDCLIAQVQEGFMSLYKGLFSLWLRMTPWSVFWLTVEKIR 315
Db 248 VMNQPRDSNGRGLLYRNSTDCLVQSVRRGFFSLYKGLFTWFRMAPSLTFLWLTPEQLR 307
Qy 316 EMSGVSPF 323
Db 308 RAMG1SSF 315

RESULT 8
Q9VX14 PRELIMINARY; PRT; 340 AA.
ID Q9VX14 AC Q9VX14;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG6492 protein
GN UCP4 OR CG6492.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.R., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam M.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabrielian A.E., Garg N.S., Geibart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DB EMBL; AF003506; AAF48769.1; -

```

```

DR FlyBase; FBgn0030872; Ucp4A.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006839; P:mitochondrial transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR002030; Mit uncoupling.
DR Pfam; PF00153; mito carr; 3.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 340 AA; 37096 MW; E452932B7C1C46D1 CRC64;

Query Match 55.2%; Score 933; DB 5; Length 340;
Best Local Similarity 57.2%; Pred. No. 3.1e-71;
Matches 174; Conservative 56; Mismatches 70; Indels 4; Gaps 2;

Qy 20 ASKFLSLGCAATVAELATPLDLTKTRLOWGGAALRLGDGAREAPYRGVMVRLALGII 79
Db 41 ACTYIVSVVAASIAELATPLDLTKTRLOIQGGAHAG--KSNMQYRGVATATAGIA 97
Qy 80 EEEGFLKMQGVTPAIYRVHVYSGGRMVTYEHURVVFGKSEDEHPLVKSIVGGMMAGV 139
Db 98 REEGALKMQGVTPALYRVHVYSGVRICSYDLMRK-EFTQGTQALPVMKSLCGVTAGA 156
Qy 140 IQGFANPTDLVKVQVQMEGRKLEKGLPRFRGVHAFKILAEAGGIRGLWAGVNVNIR 199
Db 157 VAQWLASPADLVKVQVQMEGRRLMGEPVRVHSGAHAFRQIVQVRGKGLWKGSIPIVQR 216
Qy 200 AALVNMGDLTTTDTVKHYLVNTPLENDIMTHGLSLCGLVASILGTADVIKSRIMNQ 259
Db 217 AALVNLGDLTTTDTYTIKHLIMNRLQMPDCHTVHVLASVACAGFAALMGTPADVVKTRIMNQ 276
Qy 260 PRDKQGRGLLYKSSDCLIAQVQEGFMSLYKGLFSLWLRMTPWSVFWLTVEKIREMSG 319
Db 277 PTDENGRLLYRGSVDCLAQTQVSKGVALYKGLFPCWIRMAPSLTFLWLTPEQLR 336
Qy 320 VSPF 323
Db 337 ASGY 340

RESULT 9
001883 PRELIMINARY; PRT; 324 AA.
ID 001883 AC 001883;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN K07B1.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Pauley A., Gattung S.;
RT "The sequence of C. elegans cosmid K07B1.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

```



```

Db 313 RVGPASVVFWMTEQIRRRFG 333
RESULT 11
Q9XI74
ID Q9XI74 PRELIMINARY; PRT; 305 AA.
AC Q9XI74
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE F7A19.22 protein (Putative mitochondrial uncoupling protein).
GN F7A19.22.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv, Columbia;
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RN Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RP Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 0:0-0(2002).
[3]
SEQUENCE FROM N.A.
RP Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007576; AAD39300.1; -
DR ENBL; AY084432; AAM61005.1; -
DR PIR; H86274; H86274.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006839; P:mitochondrial transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR002067; Mit carrier.
DR InterPro; IPR002030; Mit uncoupling.
DR Pfam; PF00153; mito_carr_3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
SQ SEQUENCE 305 AA; C1122C9B866BC32A CRC64;
Query Match 39.5%; Score 667.5; DB 10; Length 305;
Best Local Similarity 42.5%; Pred. No. 1.2e-48;
Matches 137; Conservative 69; Mismatches 84; Indels 33; Gaps 8;
QY 13 LTQWRPRASKFLSGCAATVAELATFPDLTKTRLMQGEAALA---RLGDGAGESAPYR 69
Db 6 VTREAPTGRILLASLSAMVAESVTFPDLTKTRMLQHGSGSAGAHRIG-----55
QY 70 GMYRTALGIER-----EGFLKLMOGVTPAIYRHVVYSGGRMVTYEHLEVRVFKSE---D 122
Db 56 -----AFGVVSEIARKEGVGLYKGLSPALIRLFTVPIRIIYENLKLIV-RSETNNS 109
QY 123 EHYPL-WKSVGMAGVIGQFLANPTDLTKVQWMEGKRKLEKGLPRFRGVHFAKIL 191
Db 110 ESPLATKALVGG-FSGVIAQVVASPADLVKVRMQADGRLVSQLGKLPFRYSGPIEAFTKIL 168

182 AEGGIRGLWAGWVPNTQRAALVNMGLTYYDTYVKHYLVLVNTPLEDNIMTHGLSLCSGLV 241
Db 169 QSEGVKGLWKGVLPTNQRAFLVNMGLACYDHAKHFVIDKKIABDNIFAHITLASMSGLA 228
QY 242 ASILGTPADVIKSRINNOPDKOGRGLLYKSSYDCLIQAVOGEGFMSLYKGFPLSWLRMT 301
Db 229 STSLSCPADVVKTRMMN-----QGENAVYRNSYDCLVTKYKFGIRGLWKGFFPTWARLG 283
QY 302 PWSMVFWLTYEKIREMSGVSPF 323
Db 284 PWQFVFWVSYEKERLLAGISSF 305

RESULT 12
Q7XTC5
ID Q7XTC5 PRELIMINARY; PRT; 314 AA.
AC Q7XTC5
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE OSJNBA0064H22.22 protein.
GN OSJNBA0064H22.22.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
SEQUENCE FROM N.A.
RA Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F.,
RA Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y.,
RA Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W.,
RA Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q.,
RA Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z.,
RA Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,
RA Lu T.T., Zhang Y.J., Du Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,
RA Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M.,
RA Zhang R.Q., Guan J.P., Hong G.F.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL606448; CAE01572.1; -
SQ SEQUENCE 314 AA; 33541 MW; 673CBB155B84F1A3 CRC64;
Query Match 37.4%; Score 632; DB 10; Length 314;
Best Local Similarity 42.5%; Pred. No. 1.3e-45;
Matches 127; Conservative 61; Mismatches 95; Indels 16; Gaps 4;
QY 21 SKFLSGCAATVAELATFPDLTKTRLMQGEAALRLDGCARESAPIRGVWRTALGIE 80
Db 22 AKVLSLSLSAAAAEAATFPDVAVKTRLELHRTGSGSGGG-----GVMRVAGELVR 73
QY 81 EEGFLKLMOGVTPAIYRHVVYSGGRMVTYEHLEVRVFKSEDEHYPLWKSIVIGMMAGVI 140
Db 74 DGG---IYRGLSPAVLRHLFYTPLRIVGVHLEHSTFASGGDA--GLLEKALAGVSGVV 128
QY 141 GQFLANPTDLVKVQWMEGKRKLEKGLPRFRGVHFAKILAEGLGIRGLWAGWVPNTQRA 200
Db 129 AQVVASPADLVKVRMQADSRLLSQIGQIPRYTGTFDAFTKIVRAEGPRGLWGVVPAQRA 188
QY 201 ALVNMGLTYYDTYVKHYLVNTPLEDNIMTHGLSLCSGLVASILGTTPADVIKSRINQOP 260
Db 189 FLVNMGLTCYDQAKHFIRKQICGNDLYAHTLASVASGLSATLSCPADVIKTRMNQO 248
QY 261 RDQKGRGLYKSSYDCLIQAVOGEGFMSLYKGFPLPSWLRMTYKREMSG 319
Db 249 KDAK---VLYRNSYDCLVTKVREHGLTALWKGLPTWARLGPWQFVFWVSYEKLQASG 304

RESULT 13
Q9CR58
ID Q9CR58 PRELIMINARY; PRT; 291 AA.
AC Q9CR58
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

```


OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OC Ephydroidea; Drosophilidae; Drosophila.
OC	NCBI_TaxID=7227;
OC	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Berkeley;
RC	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celnik S.E., Holt R.A., Hoskins R.A., Galle R.F., RA Ananides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.-H.C., Blazie R.G., Champagne M., Pfeiffer B.D., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D., RA Balow R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT	"The genome sequence of Drosophila melanogaster.";
RL	Science 287:2185-2195(2000).
RP	SEQUENCE FROM N.A.
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Faragas V., Park S., RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., RA Celnik S.;
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR	EMBL; AE003612; AAF52313.1; -
DR	EMBL; AY089345; AAL90083.1; -
DR	FlyBase; FBgn0031757; Ucp4C.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR	GO; GO:0005488; F:binding; IEA.
DR	GO; GO:0006810; P:transport; IEA.
DR	InterPro; IPR001993; Mitoch_carrier.
DR	InterPro; IPR02087; Mit_carrier.
DR	Pfam; PF00153; mito_carr; 3.
DR	PRINTS; PR00926; MITOCARRIER.
DR	PROSITE; PS00215; MITOCH_CARRIER; 3.
KW	Membrane; Transmembrane; Transport
SQ	SEQUENCE 335 AA; 38194 MW; 4750453F0828B4DE CRC64;

Matches 121; Conservative 65; Mismatches 126; Indels 14; Gaps 4;
 QY 5 EEEERLLPLTQRWRPRASK-----FLLSGCAATVAELATPFLDLTKTRLOMQGEAALARLG 59
 DB 17 EEEPRFPPTNVADPLTARNLFLQLYVNTFFGNNLAESCVPFLDVAKTRMQVDGEQAKT-- 74
 QY 60 DGARESAPYRGVMVRTALGIIIEEGFLKLMQGVTPAIYRHVVYSGGRMVTYEHLEVVFGK 119
 DB 75 --GKAMPTFRA---TLTNMIRVEGFKSLVAGFSAMVTRNFINSRLRVLYDVFRRPFLYQ 129
 QY 120 SE--DEHYPLWKSIVIGMAGVIGQFLANPTDLVKVQMQMEGKKLECKPLRRFGVHAF 177
 DB 130 NERNEEVLYKIYMALGCSFTAGCTAQAALANPFDIVKVRMQTEGRRRQGLGYDVRVNSMVQAF 189
 QY 178 AKTLAEGGIRGLWAGWVPIQRAALVNMGLTYYDTVKHYLVLENTPLEDNIMTHGLSSLC 237
 DB 190 VDIYRGGILPSMWKGVGSPCMRACLMTTGVGYSIDSKRTFKLLDLLEGLPLRFVSSMC 249
 QY 238 SGLVASILGTPADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFPLPSW 297
 DB 250 AGLTASVLTSPADVIKSRIMNQPVDESCKNLYKNSLDCVRLVREBGLVTLTKGLMPTW 309
 QY 298 LRMTPSMWFLTYEKIREMSGVSPF 323
 DB 310 FRLGPFSEVLFWSVEQLRQWEGOSGF 335

Search completed: September 24, 2004, 03:56:33
 Job time : 90 secs

Query Match 32.9%; Score 556; DB 5; Length 335;
 Best Local Similarity 37.1%; Pred. No. 4.5e-39;

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2004, 03:58:39 ; Search time 4096 Seconds
(without alignments)
10994.485 Million cell updates/sec

Title: US-09-397-342C-2
Perfect score: 1039
Sequence: 1 ccgagctcgatcccgcttat.....cagatatccatcacactggc 1039

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.man.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1039	100.0	1039	6	BD233771	BD233771 UCp4. 7/2
2	998	96.1	998	6	AX092394	AX092394 Sequence
3	998	96.1	998	6	AX697337	AX697337 Sequence
4	998	96.1	998	9	AY358711	AY358711 Homo sapi
5	990.6	95.3	1248	6	BD233774	BD233774 UCp4. 7/2
6	972	93.6	972	6	AX269363	AX269363 Sequence
7	972	93.6	972	9	AF110532	AF110532 Homo sapi
8	793	76.3	2851	10	AB106930	AB106930 Mus muscu
9	785	75.6	2678	10	RNO300162	AJ300162 Rattus no
10	729.6	70.2	1339	9	BC033091	BC033091 Homo sapi
11	716.8	69.0	1890	10	RNO300164	AJ300164 Rattus no
12	715.2	68.8	2620	10	RNO300163	AJ300163 Rattus no
13	676.8	65.1	1726	6	AX061217	AX061217 Sequence
14	676.8	65.1	3266	6	AX746657	AX746657 Sequence
15	676.8	65.1	3266	9	AK090871	AK090871 Homo sapi
16	435.8	41.9	1295	5	BC053139	BC053139 Danio rer
17	322.6	31.0	2118	3	AK114236	AK114236 Ciona int
18	234.8	22.6	1546	3	AK115101	AK115101 Ciona int
19	194.6	18.7	18042	9	AL590794	AL590794 Human DNA
20	194.6	18.7	95107	9	AL591242	AL591242 Human DNA
21	165.8	16.0	228	6	AX331480	AX331480 Sequence
22	156.6	15.1	200860	2	AC112993	AC112993 Mus muscu
23	156.6	15.1	237804	2	AC120552	AC120552 Mus muscu
24	150.2	14.5	227939	2	AC125648	AC125648 Rattus no
25	150.2	14.5	229218	2	AC107523	AC107523 Rattus no
26	150.2	14.5	233492	2	AC111723	AC111723 Rattus no
27	140	13.5	1071	8	AY084432	AY084432 Arabidops
28	137.2	13.2	1315	8	AK064234	AK064234 Oryza sat
29	136.6	13.1	945	6	AX653527	AX653527 Sequence
30	134	12.9	566	9	HS3334577	AJ334577 Homo sapi
31	134	12.9	567	9	HS3334578	AJ334578 Homo sapi
32	132.4	12.7	1209	8	AB088762	AB088762 Helicodic
33	130.8	12.6	1126	8	AK105976	AK105976 Oryza sat
34	130.6	12.6	147214	8	OSUN00013	AL606448 Oryza sat
35	124	11.9	1083	8	AK117673	AK117673 Arabidops
36	124	11.9	112126	8	AC007576	AC007576 Arabidops
37	117.4	11.3	1525	6	E50743	E50743 Plant exoth
38	117.4	11.3	1525	6	BD011855	BD011855 Thermogen
39	117.4	11.3	1525	8	AB024733	AB024733 Symplocar
40	116.2	11.2	1434	8	STUCPMRNA	Y11250 Solanum tub
41	116	11.2	169457	2	AC009216	AC009216 Drosophil
42	116	11.2	169856	3	AC012162	AC012162 Drosophil
43	116	11.2	302073	3	AE003506	AE003506 Drosophil
44	115	11.1	1240	8	ATMTUNCOU	AJ001264 Arabidops
45	114.6	11.0	1429	8	AF472619	AF472619 Lycopersi

ALIGNMENTS

RESULT 1	BD233771	BD233771	1039 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	UCP4.					
DEFINITION	BD233771					
ACCESSION	BD233771	GI:33043541				
VERSION	JP 2002526075-A/1.					
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
REFERENCE	1 (bases 1 to 1039)					
AUTHORS	Adams,S., Fan,J. and Zhong,A.					
TITLE	UCP4					
JOURNAL	Patent: JP 2002526075-A 1 20-AUG-2002;					

GENENTECH INC	OS	Homo sapiens (human)																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
---------------	----	----------------------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

Db	181	AAGCAGCTCTTGCTCGTGGGAGACGGTCAAGAGAATCTGCCCTATAGGGGAATGG	240
Qy	254	TGGCAGAGCCCTAGGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA	313
Db	241	TGGCAGAGCCCTAGGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA	300
Qy	314	CACCGCCATTTCACAGACAGTGTATTTCTGGAGTCAATGGTGCATATATGAACATC	373
Db	301	CACCGCCATTTCACAGACAGTGTATTTCTGGAGTCAATGGTGCATATATGAACATC	360
Qy	374	TCCGAGAGGTGTGTTGGGCAAGTCAAGATGAGCATTTATCCCTTTGGAAATCAGTCA	433
Db	361	TCCGAGAGGTGTGTTGGGCAAGTCAAGATGAGCATTTATCCCTTTGGAAATCAGTCA	420
Qy	434	TTGGAGGATGATGGCTGTGTTATTTGGCCAGTCTTTAGGCAATCCAACTGACCTAGTGA	493
Db	421	TTGGAGGATGATGGCTGTGTTATTTGGCCAGTCTTTAGGCAATCCAACTGACCTAGTGA	480
Qy	494	AGTTTCAGATGCAAAATGGAAAGGAAAGAACTGGAAAGGAAACCAATTCGGATTCGTC	553
Db	481	AGTTTCAGATGCAAAATGGAAAGGAAAGAACTGGAAAGGAAACCAATTCGGATTCGTC	540
Qy	554	GTGTACATCATGCTATTTGCAAAATCTTACGAGGAGCAATTCAGGAGGAGGAGGAGG	613
Db	541	GTGTACATCATGCTATTTGCAAAATCTTACGAGGAGCAATTCAGGAGGAGGAGGAGG	600
Qy	614	GCTGGGTACCAATATACAAAGAGCAGCACTGTGTGAATATGGGAGATTTAAACCACTATG	673
Db	601	GCTGGGTACCAATATACAAAGAGCAGCACTGTGTGAATATGGGAGATTTAAACCACTATG	660
Qy	674	ATACAGTGAACACTACTTGGTATTCGATACACCACTTGGAGGAGCAATATCATGACTCACG	733
Db	661	ATACAGTGAACACTACTTGGTATTCGATACACCACTTGGAGGAGCAATATCATGACTCACG	720
Qy	734	GTATTCAAGTATTTATGTTCTGGAGTGGTATTCGATACCACTTGGAGGAGCAATATCATGACTCACG	793
Db	721	GTATTCAAGTATTTATGTTCTGGAGTGGTATTCGATACCACTTGGAGGAGCAATATCATGACTCACG	780
Qy	794	TCAAAAGCAGAAATTAATGAATCAACACGAGATTAACCAAGGAGGAGGAGGAGGAGG	853
Db	781	TCAAAAGCAGAAATTAATGAATCAACACGAGATTAACCAAGGAGGAGGAGGAGGAGG	840
Qy	854	CATCGACTGACTGCTTGTATTCAGGCTGTTCAAGGTGAGGATTCATGAGTCTATATAAG	913
Db	841	CATCGACTGACTGCTTGTATTCAGGCTGTTCAAGGTGAGGATTCATGAGTCTATATAAG	900

JOURNAL	Patent: WO 0078961-A 405 28-DEC-2000;									
Genentech Inc. (US)										
FEATURES	Location/Qualifiers									
source	1..998									
	/organism="Homo sapiens"									
	/mol_type="unassigned DNA"									
	/db_xref="taxon:9606"									
ORIGIN										
Query Match	96.1%; Score 998; DB 6; Length 998;									
Best Local Similarity	100.0%; Pred. No. 2.3e-275; Indels 0; Gaps 0;									
Matches 998; Conservative	0; Mismatches 0; Indels 0; Gaps 0;									
Qy	14	CCGTTATCGCTTTCGCGTACTGTCTGTAATGTCCGTC	CCGAGGAGGAGGAGGAGGCTTTTGC	73						
Db	1	CCGTTATCGCTTTCGCGTACTGTCTGTAATGTCCGTC	CCGAGGAGGAGGAGGAGGCTTTTGC	60						
Qy	74	CGCTGACCCAGAGATGGCCCGGAGCGAGCAAAATCT	CTACTGTCCGGCTGCGCGCTACCG	133						
Db	61	CGCTGACCCAGAGATGGCCCGGAGCGAGCAAAATCT	CTACTGTCCGGCTGCGCGCTACCG	120						
Qy	134	TGGCCGAGCTAGCAACCTTTTCCCTCTGATCTCA	CAAAAATCTCGACTCCAAATGCAAGGAG	193						
Db	121	TGGCCGAGCTAGCAACCTTTTCCCTCTGATCTCA	AAAAATCTCGACTCCAAATGCAAGGAG	180						
Qy	194	AAGCAGCTCTTGTCTCGGTTGGGAGACGGTCA	AGAGAATCTGCCCTCTATAGGGGAATGG	253						
Db	181	AAGCAGCTCTTGTCTCGGTTGGGAGACGGTCA	AGAGAATCTGCCCTCTATAGGGGAATGG	240						
Qy	254	TGGCGACAGCCCTAGGATCATTTGAAGAGGAAGCT	TTCTAAAGCTTTGGCAAGGAGTGA	313						
Db	241	TGGCGACAGCCCTAGGATCATTTGAAGAGGAAGCT	TTCTAAAGCTTTGGCAAGGAGTGA	300						
Qy	314	CACCCGCCATTTACAGACACGTAGTGTATTTCT	GGAGTCAATATGGTGCATATGAACATC	373						
Db	301	CACCCGCCATTTACAGACACGTAGTGTATTTCT	GGAGTCAATATGGTGCATATGAACATC	360						
Qy	374	TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATG	AGCAATTCCTCTTTGGAAATCAGTCA	433						
Db	361	TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATG	AGCAATTCCTCTTTGGAAATCAGTCA	420						
Qy	434	TTGGAGGGATGATGGCTGTGTTATTTGGCCAGT	TTTTAGGCAATCCAACTGACCTAGTGA	493						
Db	421	TTGGAGGGATGATGGCTGTGTTATTTGGCCAGT	TTTTAGGCAATCCAACTGACCTAGTGA	480						
Qy	494	AGGTTTCAGATGCAAAATGGAAAGGAAAGAA	CTGGAAAGGAAACCAATTCGGATTCGTCG	553						
Db	481	AGGTTTCAGATGCAAAATGGAAAGGAAAGAA	CTGGAAAGGAAACCAATTCGGATTCGTCG	540						
Qy	554	GTGTACATCATGCTATTTGCAAAAATCTTAC	TGAGGAGGAATACGAGGGCTTTGGGCAG	613						
Db	541	GTGTACATCATGCTATTTGCAAAAATCTTAC	TGAGGAGGAATACGAGGGCTTTGGGCAG	600						
Qy	614	GCTGGGTACCAATATACAAAGAGCAGCACTGT	GTAATATGGGAGATTTAAACCACTTATG	673						
Db	601	GCTGGGTACCAATATACAAAGAGCAGCACTGT	GTAATATGGGAGATTTAAACCACTTATG	660						
Qy	674	ATACAGTGAACACTACTTGGTATTCGAATAC	CCACTTTGAGGAGCAATATCATGACTCACG	733						
Db	661	ATACAGTGAACACTACTTGGTATTCGAATAC	CCACTTTGAGGAGCAATATCATGACTCACG	720						
Qy	734	GTATTATCAAGTTTATGTTCTGGACTGGTAT	CTCTATTCTTGGGAAACCAACGACCGATGCA	793						
Db	721	GTATTATCAAGTTTATGTTCTGGACTGGTAT	CTCTATTCTTGGGAAACCAACGACCGATGCA	780						
Qy	794	TCAAAAGCAGAAATAATGAATCAACACGAGAT	TAAACAAAGGAAGGGGACTTTTGTATATAAT	853						
Db	781	TCAAAAGCAGAAATAATGAATCAACACGAGAT	TAAACAAAGGAAGGGGACTTTTGTATATAAT	840						
Qy	854	CATCGACTGACTGCTTGTATTCAGGCTGTTT	CAAGGTGAGGATTCATGAGTCTATATAAG	913						
Db	841	CATCGACTGACTGCTTGTATTCAGGCTGTTT	CAAGGTGAGGATTCATGAGTCTATATAAG	900						

RESULT 3

LOCUS	AX697337	998 bp	DNA	linear	PAT 02-APR-2003
DEFINITION	Sequence 405 from Patent WO0078961.				
ACCESSION	AX697337				
VERSION	AX697337.1	GI:29498472			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L., Eaton, D.L., Gao, W.Q., Pan, J., Botstein, D., Fong, S., Goddard, A., Godowski, P.J., Gurney, A.L., Smith, V., Tumas, D., Wood, W.I., Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A., and Watanabe, C.K.				
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same				

QY 914 GCTTTTACCATTCTGGCTGAGAAAGCCCTTGGTCAATGGTCTTCTGGCTTACTTATG 973
 DB 901 GCTTTTACCATTCTGGCTGAGAAAGCCCTTGGTCAATGGTCTTCTGGCTTACTTATG 960
 QY 974 AAAAAATCAGAGAGATGAGTGGAGTCACTGCTCCATTTTAA 1011
 DB 961 AAAAAATCAGAGAGATGAGTGGAGTCACTGCTCCATTTTAA 998

RESULT 4
 AY358711 998 bp mRNA linear PRI 03-OCT-2003
 LOCUS Homo sapiens DNA77568 UCP4 (UNQ772) mRNA, complete cds.
 DEFINITION AY358711
 ACCESSION AY358711
 VERSION AY358711.1 GI:37182543
 KEYWORDS FLI_CDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 998); Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vanden,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
 TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
 JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
 PUBMED 12975309
 REFERENCE 2 (bases 1 to 998)
 AUTHORS Clark,H.F.
 DIRECT SUBMISSION
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES
 source
 1..998
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DNA77568"
 1..998
 /locus_tag="UNQ772"
 27..998
 /locus_tag="UNQ772"
 /notes="PRO1566"
 /codon_start=1
 /product="UCP4"
 /protein_id="AAQ89951.1"
 /db_xref="GI:3722206"
 /translation="MSVPDEERLLPLTORWPRASKFLSGCAATVAELATPLDLTK
 TRLQMGEEALRLGPGARESAPYRGWVRLTGLIEEGFLKIQCVTALIRHVYVS
 GGRMVTYHLRVFVFKSDEHYPLWKSIVIGNMAGVIGQFLNFDLVKVMQMEGK
 RKLGEPLFRGVHFAKILAEGRIGLWAGVNPVQRAALVNMGLDLYDTVRHYL
 VLNPLEDMIMTHLSLCSGLVASILGTPADVIKIRIMNPQDKGRLLYKSTDC
 LIQAVQEGFMSLYKGLFSLWLRTPWSNVFMLTYEKIREMSGVSPF"

gene
 CDS
 1..998
 /locus_tag="UNQ772"
 27..998
 /locus_tag="UNQ772"
 /notes="PRO1566"
 /codon_start=1
 /product="UCP4"
 /protein_id="AAQ89951.1"
 /db_xref="GI:3722206"
 /translation="MSVPDEERLLPLTORWPRASKFLSGCAATVAELATPLDLTK
 TRLQMGEEALRLGPGARESAPYRGWVRLTGLIEEGFLKIQCVTALIRHVYVS
 GGRMVTYHLRVFVFKSDEHYPLWKSIVIGNMAGVIGQFLNFDLVKVMQMEGK
 RKLGEPLFRGVHFAKILAEGRIGLWAGVNPVQRAALVNMGLDLYDTVRHYL
 VLNPLEDMIMTHLSLCSGLVASILGTPADVIKIRIMNPQDKGRLLYKSTDC
 LIQAVQEGFMSLYKGLFSLWLRTPWSNVFMLTYEKIREMSGVSPF"

Query Match 96.1%; Score 998; DB 9; Length 998;
 Best Local Similarity 100.0%; Pred. No. 2.3e-275;
 Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCCTTATCGCTTTCGCTACTGCTGAATGTCCTCCCGGAGGAGGAGAGGCTTTTCG 73
 DB 1 CCCTTATCGCTTTCGCTACTGCTGAATGTCCTCCCGGAGGAGGAGAGGCTTTTCG 60

QY 74 CGCTGACCCAGAGATGCGCCGAGGAGCAAAATCTACTGCTCGGCTGGCGGCTACCG 133
 DB 74 CGCTGACCCAGAGATGCGCCGAGGAGCAAAATCTACTGCTCGGCTGGCGGCTACCG 133

ORIGIN

Query Match 96.1%; Score 998; DB 9; Length 998;
 Best Local Similarity 100.0%; Pred. No. 2.3e-275;
 Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 61 CGCTGACCCAGAGATGCGCCGAGGAGCAAAATCTACTGCTCGGCTGGCGGCTACCG 120
 QY 134 TGGCCGAGCTAGCAACCTTTCCCTCGGATCTCAAAAAAATCTCGACTCAAAATGCAAGGAG 193
 DB 121 TGGCCGAGCTAGCAACCTTTCCCTCGGATCTCAAAAAAATCTCGACTCAAAATGCAAGGAG 180
 QY 194 AAGCAGCTCTTCTCGGCTGGGAGACGGTGCAGAGAAATCTGCCCTCTATAGGGGAATGG 253
 DB 181 AAGCAGCTCTTCTCGGCTGGGAGACGGTGCAGAGAAATCTGCCCTCTATAGGGGAATGG 240
 QY 254 TGGCGCAGCCCTAGGAGTCAATGAGAGGAAGGCTTTCTAAAGCTTTGCAAGGAGTGA 313
 DB 241 TGGCGCAGCCCTAGGAGTCAATGAGAGGAAGGCTTTCTAAAGCTTTGCAAGGAGTGA 300
 QY 314 CACCCGCCATTACAGACACGCTAGTGTATTTCTGGAGGTGGAATGGTGCATATGAACATC 373
 DB 301 CACCCGCCATTACAGACACGCTAGTGTATTTCTGGAGGTGGAATGGTGCATATGAACATC 360
 QY 374 TCCGAGAGGTTGTTTGGCAAAAGTGAAGATGAGCATTTATCCCTTTGGAAATCAGTCA 433
 DB 361 TCCGAGAGGTTGTTTGGCAAAAGTGAAGATGAGCATTTATCCCTTTGGAAATCAGTCA 420
 QY 434 TTGGAGGATGATGGCTGGTGTATTATGGCCAGTCTTTTAGCCCAATCCAACTGACCTAGTGA 493
 DB 421 TTGGAGGATGATGGCTGGTGTATTATGGCCAGTCTTTTAGCCCAATCCAACTGACCTAGTGA 480
 QY 494 AGGTTTCAGATGCAAAATGGAAGGAAAAAGGAAATCTGGAAGGAAAAACCAATTCGATTCGTTG 553
 DB 481 AGGTTTCAGATGCAAAATGGAAGGAAAAAGGAAATCTGGAAGGAAAAACCAATTCGATTCGTTG 540
 QY 554 GTGTACATCATGCTTTGCAAAAAATCTTAGTGAAGGAGAAATACAGGGCTTTGGGCGAG 613
 DB 541 GTGTACATCATGCTTTGCAAAAAATCTTAGTGAAGGAGAAATACAGGGCTTTGGGCGAG 600
 QY 614 GCTGGGTACCCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 673
 DB 601 GCTGGGTACCCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 660
 QY 674 ATACAGTAAAAACACTACTTGGTATGAAATACACCACTTGAAGGACAAATATCATGACTCACG 733
 DB 661 ATACAGTAAAAACACTACTTGGTATGAAATACACCACTTGAAGGACAAATATCATGACTCACG 720
 QY 734 GTTTATCAAGTTTATGTTCTGACCTGGTACTTCTTATCTGGGAAACACAGCGGATGTCA 793
 DB 721 GTTTATCAAGTTTATGTTCTGACCTGGTACTTCTTATCTGGGAAACACAGCGGATGTCA 780
 QY 794 TCAAAAGCAGAATAATGAATCAACACGAGATAAAACAGGAAGGGGACTTTTGTATAAAT 853
 DB 781 TCAAAAGCAGAATAATGAATCAACACGAGATAAAACAGGAAGGGGACTTTTGTATAAAT 840
 QY 854 CATCGACTGACTGCTTGAATTCAGGCTGTTTCAAGGTGAAGGATTCATGAGTCTATATAAAG 913
 DB 841 CATCGACTGACTGCTTGAATTCAGGCTGTTTCAAGGTGAAGGATTCATGAGTCTATATAAAG 900
 QY 914 GCTTTTACCATCTTGGCTGAGAATGACCCCTTGGTCAATGCTGCTGCTTACTTATG 973
 DB 901 GCTTTTACCATCTTGGCTGAGAATGACCCCTTGGTCAATGCTGCTGCTTACTTATG 960
 QY 974 AAAAAATCAGAGAGATGAGTGGAGTCACTGCTCCATTTTAA 1011
 DB 961 AAAAAATCAGAGAGATGAGTGGAGTCACTGCTCCATTTTAA 998

RESULT 5

BD233774
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BD233774 1248 bp DNA linear PAT 17-JUL-2003
 UCP4.
 BD233774
 BD233774.1 GI:33043544
 JP 2002526075-A/4.
 synthetic construct
 synthetic construct
 artificial sequences.

```
REFERENCE 1 (bases 1 to 1248)
AUTHORS Adams,S., Pan,J. and Zhong,A.
TITLE UCP4
JOURNAL GENENTECH INC
COMMENT OS Artificial Sequence
PN PD 20-SEP-1998 US 60/101279,30-DEC-1998 US 60/114223 PR
PR 15-SEP-1999 JP 2000574252
PR 22-SEP-1998 US 60/129674
16-APR-1999 US 60/129674
PI SEAN ADAMS, JAMES PAN, ALAN ZHONG
PC C12N15/09,A61K45/00,A61P3/00,A61P3/04,C07K14/47,C07K16/18, PC
C07K19/00,
PC C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12Q1/02,C12Q1/68,G01N33/
68//
PC (C12N1/19,C12R1:865), (C12N1/21,C12R1:19), (C12P21/02,C12R1:19),
PC (C12P21/02,C12R1:865), (C12P21/02,C12R1:91), (C12N15/00,C12N5/00
CC Artificial Sequence 1-1248
unknown base
FH Key Location/Qualifiers
FT unsure 1231.
Location/Qualifiers
1..1248
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 95.3%; Score 990.6; DB 6; Length 1248;
Best Local Similarity 99.6%; Pred. No. 3.2e-273;
Matches 993; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 15 CGTTATCGTCTCGGCTACTGCTGAATGTCGTCGCGGAGGAGGAGGAGGCTTTTGCC 74
Db 1 CGTTATCGTCTCGGCTACTGCTGAATGTCGTCGCGGAGGAGGAGGAGGCTTTTGCC 60

QY 75 GCTGACCCAGAGATGGCCCGAGGAGCAAAATTCCTACTGTCGCGGCTGCGCGGTACCGT 134
Db 61 GCTGACCCAGAGATGGCCCGAGGAGCAAAATTCCTACTGTCGCGGCTGCGCGGTACCGT 120

QY 135 GCGGAGCTAGCAACCTTTCCCTCGATCTCAAAAATCGATCGCAAAATGCAAGAGA 194
Db 121 GCGGAGCTAGCAACCTTTCCCTCGATCTCAAAAATCGATCGCAAAATGCAAGAGA 180

QY 195 AGCAGCTCTTCTCGGTTGGGAGACGCTGCAAGAGATCTGCCCTATAGGGGAATGGT 254
Db 181 AGCAGCTCTTCTCGGTTGGGAGACGCTGCAAGAGATCTGCCCTATAGGGGAATGGT 240

QY 255 GCGCAGACGCTAGGGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTGCAAGGAGTGAC 314
Db 241 GCGCAGACGCTAGGGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTGCAAGGAGTGAC 300

QY 315 ACCCGCATTTACAGACACCTAGTGATTTCTGAGGTGCAATGCTGCAATGCAACATCT 374
Db 301 ACCCGCATTTACAGACACCTAGTGATTTCTGAGGTGCAATGCTGCAATGCAACATCT 360

QY 375 CCGAGAGTTGCTTTGGCAAAAGTGAAGTGAATGAGCATTTCCCTTTGGAATCAGTCAT 434
Db 361 CCGAGAGTTGCTTTGGCAAAAGTGAAGTGAATGAGCATTTCCCTTTGGAATCAGTCAT 420

QY 435 TGAGGGATGATGGCTGGTGTATTTGGCCAGTTTATTTAGCCAAATCCCACTAGTGAA 494
Db 421 TGAGGGATGATGGCTGGTGTATTTGGCCAGTTTATTTAGCCAAATCCCACTAGTGAA 480

QY 495 GGTTCAGATGCAATGGAAGGAAAAAGAACTGGAAGGAAAAACCAATTCGATTTCTGG 554
Db 481 GGTTCAGATGCAATGGAAGGAAAAAGAACTGGAAGGAAAAACCAATTCGATTTCTGG 540

QY 555 TGTACATCATGCTTTGCAAAATCTTAGCTGAAGGAGGATACGAGGCTTTGGCAGG 614
Db 541 TGTACATCATGCTTTGCAAAATCTTAGCTGAAGGAGGATACGAGGCTTTGGCAGG 600

QY 615 CTGGGTACCCCAATATACAAAGAGCAGCAGCTGGTGAATATGGGAGATTAAACCATTAGA 674
Db 601 CTGGGTACCCCAATATACAAAGAGCAGCAGCTGGTGAATATGGGAGATTAAACCATTAGA 660

QY 675 TACAGTGAACACTACTTGGTATTGAATACACCACTTGAGGACAAATATCATGACTCAGG 734
Db 661 TACAGTGAACACTACTTGGTATTGAATACACCACTTGAGGACAAATATCATGACTCAGG 720

QY 735 TTTTCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAAGCCGATGTCAT 794
Db 721 TTTTCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAAGCCGATGTCAT 780

QY 795 CAAAAGCAGAAATATGAATCAACACGAGATAAACAAAGAAAGGAGACTTTTGTATAAATC 854
Db 781 CAAAAGCAGAAATATGAATCAACACGAGATAAACAAAGAAAGGAGACTTTTGTATAAATC 840

QY 855 ATCGACTGACTGCTTCAATTCAGGCTGTTCAAGTGAAGGATTCATGAGTCTATATAAGG 914
Db 841 ATCGACTGACTGCTTCAATTCAGGCTGTTCAAGTGAAGGATTCATGAGTCTATATAAGG 900

QY 915 CTTTTTACCATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATGA 974
Db 901 CTTTTTACCATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATGA 960

QY 975 AAAAAATCAGAGAGATGAGTGGAGTCACTCAGTCCATTTAA 1011
Db 961 AAAAAATCAGAGAGATGAGTGGAGTCACTCAGTCCATTTAA 997

RESULT 6
AX269363
LOCUS AX269363
DEFINITION Sequence 10 from Patent WO0175131.
ACCESSION AX269363
VERSION AX269363.1 GI:16542178
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Berry-Lowe,S.L. and Newell,M.K.
TITLE Compositions and methods for regulating metabolism in plants
JOURNAL Patent: WO 0175131-A 10 11-OCT-2001;
University Technology Corporation (US)
FEATURES
source 1..972
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 93.6%; Score 972; DB 6; Length 972;
Best Local Similarity 100.0%; Pred. No. 6.9e-268;
Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 ATGTCGCTCCCGAGGAGGAGGAGGCTTTTCCCGCTGACCCAGAGATGCCCCGAGCG 99
Db 1 ATGTCGCTCCCGAGGAGGAGGAGGCTTTTCCCGCTGACCCAGAGATGCCCCGAGCG 60

QY 100 AGCAAAATTCCTACTGTCGCGGCTGCGGGCTTACCGTGGCCGAGCTAGCAACCTTTCCCTG 159
Db 61 AGCAAAATTCCTACTGTCGCGGCTGCGGGCTTACCGTGGCCGAGCTAGCAACCTTTCCCTG 120

QY 160 GATCTCAGAAAACTCGACTCCAAATGCAAGGAGAAAGAGCTCTTGTCTCGGTGGGAGAC 219
Db 121 GATCTCAGAAAACTCGACTCCAAATGCAAGGAGAAAGAGCTCTTGTCTCGGTGGGAGAC 180

QY 220 GGTGCAAGAGAACTCCCGCTTATAGGGAAATGCTGGCGACACGCCCTTAGGGATCATTTAA 279
Db 181 GGTGCAAGAGAACTCCCGCTTATAGGGAAATGCTGGCGACACGCCCTTAGGGATCATTTAA 240

QY 280 GAGGAAGGCTTTCTAAAGCTTTTGGCAAGGAGTGACACACCCGCCATTTACAGACACGTAGTG 339
```

Db 241 GAGGAAGGCTTTCTAAAGCTTTGGCAAGAGTGACACCCGCAATTACAGACAGTAGTG 300
 QY 340 TATTCTGAGGTGCAATGGTACATATGAAATCTCCGAGAGGTGTGTTGGCAAAAGT 399
 Db 301 TATTCTGAGGTGCAATGGTACATATGAAATCTCCGAGAGGTGTGTTGGCAAAAGT 360
 QY 400 GAAGATGAGCATTTCCCTTTTGAATTCAGTTCATTTGGAGGATGATGGCTGTATT 459
 Db 361 GAAGATGAGCATTTCCCTTTTGAATTCAGTTCATTTGGAGGATGATGGCTGTATT 420
 QY 460 GGCCAGTTTATAGCCCAATCCAACCTGACCTAGTAGAGGTTCAGATGCAAAATGGAAGGAAA 519
 Db 421 GGCCAGTTTATAGCCCAATCCAACCTGACCTAGTAGAGGTTCAGATGCAAAATGGAAGGAAA 480
 QY 520 AGGAATCTGGAAGAAACCAATGGATTTGGTGTGATCATATGATGCAATTTGCAAAATC 579
 Db 481 AGGAATCTGGAAGAAACCAATGGATTTGGTGTGATCATATGATGCAATTTGCAAAATC 540
 QY 580 TTAGCTGAAGGAGGAATACGAGGCTTTGGCAGGCTGGGTACCCCAATATACAAAGAGCA 639
 Db 541 TTAGCTGAAGGAGGAATACGAGGCTTTGGCAGGCTGGGTACCCCAATATACAAAGAGCA 600
 QY 640 GCATGTGATATGGAGATTTAAACCACTTATGATACAGTGAACACTACTTGTGATTG 699
 Db 601 GCATGTGATATGGAGATTTAAACCACTTATGATACAGTGAACACTACTTGTGATTG 660
 QY 700 AATACACCACTTGAGGACATATCATGACTCAGGCTTTATCAAGTTTATGTTCTGAGCTG 759
 Db 661 AATACACCACTTGAGGACATATCATGACTCAGGCTTTATCAAGTTTATGTTCTGAGCTG 720
 QY 760 GTAGCTTCTATTCTGGGAACACCAAGCGGCTGTCATCAAAAGCAGAAATGAATCAACCA 819
 Db 721 GTAGCTTCTATTCTGGGAACACCAAGCGGCTGTCATCAAAAGCAGAAATGAATCAACCA 780
 QY 820 CGAGATAAACAGGAAGGAGCTTTGTATAAATCATGCTGCTGCTGATTCAGGCT 879
 Db 781 CGAGATAAACAGGAAGGAGCTTTGTATAAATCATGCTGCTGCTGATTCAGGCT 840
 QY 880 GTTCAAGGTGAGGATTCATGAGTCTATATAAGGCTTTTACCATCTTGGCTGAGATG 939
 Db 841 GTTCAAGGTGAGGATTCATGAGTCTATATAAGGCTTTTACCATCTTGGCTGAGATG 900
 QY 940 ACCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGTGGAGTC 999
 Db 901 ACCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGTGGAGTC 960
 QY 1000 AGTCCATTTAA 1011
 Db 961 AGTCCATTTAA 972

RESULT 7
 AF110532
 LOCUS
 DEFINITION
 Homo sapiens uncoupling protein UCP-4 mRNA, nuclear gene encoding mitochondrial protein, complete cds.
 AF110532
 VERSION
 AF110532.1 GI:4324700
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 972)
 MAO, W., YU, X. X., ZHONG, A., LI, W., BRUSH, J., SHERWOOD, S. W., ADAMS, S. H. and PAN, G.
 UCP4, a novel brain-specific mitochondrial protein that reduces membrane potential in mammalian cells
 FEBS Lett. 443 (3), 326-330 (1999)
 99149824
 MEDLINE
 10025957
 PUBMED
 2 (bases 1 to 972)

AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 1. 972
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6p11.2-q12"
 /tissue_type="brain"
 1. 972
 /function="uncouples respiration in mammalian cells"
 /note="novel member of the mitochondrial carrier protein superfamily; contains six putative transmembrane domains and a putative nucleotide binding domain"
 /codon_start=1
 /product="uncoupling protein UCP-4"
 /protein_id="A016995.1"
 /db_xref="GI:4324701"
 /translation="MSVPEEERLLPLTORPRASKLLSGCAATVAELATFLDLTK
 TRLMQGEAALRLGDGARESEYPRGMVRLTALGIIIEEGFLKLWQVTVAIYRVVYS
 GRMVTVHLREWFVKSDHEVPLWKSIVGMWVNIQRAALVNMGLDLYVDVTKHVL
 RLEGGPLRPRGVHAFKILAEGRIRGLWAGWPNVIRAAVNMGLDLYVDVTKHVL
 VLNPLEDINMTGLSSLCGLVASILGTPADVIKSRIMNQPRDKQGRGLLYKSDTC
 LIQVQGEFMSLYKGLFLSWLRLMTWPSWFWLTYEKIREMSVSPF"

ORIGIN
 Query Match 93.6%; Score 972; DB 9; Length 972;
 Best Local Similarity 100.0%; Pred. No. 6,9e-268;
 Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 40 ATGTCCGTCCTCGAGAGGAGGAGGCTTTTGGCCGCTGACCCAGAGATGGCCCGAGCG 99
 Db 1 ATGTCCGTCCTCGAGAGGAGGAGGCTTTTGGCCGCTGACCCAGAGATGGCCCGAGCG 60
 QY 100 AGCAAAATCTACTGTCGCGCTGCGCGCTTACCGTGGCGGAGTACCACTTTTCCCTG 159
 Db 61 AGCAAAATCTACTGTCGCGCTGCGCGCTTACCGTGGCGGAGTACCACTTTTCCCTG 120
 QY 160 GATCTCACAATACTCGACTCCAAATGCAAGGAGAGAGCTTCTGCTCGTTGGGAGAC 219
 Db 121 GATCTCACAATACTCGACTCCAAATGCAAGGAGAGAGCTTCTGCTCGTTGGGAGAC 180
 QY 220 GGTGCAAGAGATCTGCCCCCTATAGGGAATGGTGGCAGACCCCTAGGATCATTTGAA 279
 Db 181 GGTGCAAGAGATCTGCCCCCTATAGGGAATGGTGGCAGACCCCTAGGATCATTTGAA 240
 QY 280 GAGGAAGGCTTTCTAAAGCTTTGGCAAGAGTGACACCCGCAATTTACAGACAGTAGTG 339
 Db 241 GAGGAAGGCTTTCTAAAGCTTTGGCAAGAGTGACACCCGCAATTTACAGACAGTAGTG 300
 QY 340 TATTCTGAGGTGCAATGGTACATATGAACATCTCCGAGAGGTGTGTTGGCAAAAGT 399
 Db 301 TATTCTGAGGTGCAATGGTACATATGAACATCTCCGAGAGGTGTGTTGGCAAAAGT 360
 QY 400 GAAGATGAGCATTTCCCTTTTGAATTCAGTTCATTTGGAGGATGATGGCTGTATT 459
 Db 361 GAAGATGAGCATTTCCCTTTTGAATTCAGTTCATTTGGAGGATGATGGCTGTATT 420
 QY 460 GGCCAGTTTATAGCCCAATCCAACCTGACCTAGTAGAGGTTCAGATGCAAAATGGAAGGAAA 519
 Db 421 GGCCAGTTTATAGCCCAATCCAACCTGACCTAGTAGAGGTTCAGATGCAAAATGGAAGGAAA 480
 QY 520 AGGAATCTGGAAGAAACCAATGGATTTGGTGTGATCATATGATGCAATTTGCAAAATC 579
 Db 481 AGGAATCTGGAAGAAACCAATGGATTTGGTGTGATCATATGATGCAATTTGCAAAATC 540
 QY 580 TTAGCTGAAGGAGGAATACGAGGCTTTGGCAGGCTGGGTACCCCAATATACAAAGAGCA 639
 Db 541 TTAGCTGAAGGAGGAATACGAGGCTTTGGCAGGCTGGGTACCCCAATATACAAAGAGCA 600


```
Qy 640 GCACCTGGTGAATATGGAGAGATTTAAACCACTTATGATACAGTGAACCACTACTTTGGTATTG 699
Db 601 GCACCTGGTGAATATGGAGAGATTTAAACCACTTATGATACAGTGAACCACTACTTTGGTATTG 660
Qy 700 AATACACCACTTGGAGCAATATATGACACTCAGGTTTATCAAGTTTATGTTTCTGAGCTG 759
Db 661 AATACACCACTTGGAGCAATATATGACACTCAGGTTTATCAAGTTTATGTTTCTGAGCTG 720
Qy 760 GTAGCTTCTTATTTCTGGGAACACACAGCCGATGTCTCAAAAAGCAGAAATAATGAATCAACCA 819
Db 721 GTAGCTTCTTATTTCTGGGAACACACAGCCGATGTCTCAAAAAGCAGAAATAATGAATCAACCA 780
Qy 820 CGAGATAAACAGAAAGGAGCTTTTGTATATAATCATATGATCGACTGCTTTGATTCAGGCT 879
Db 781 CGAGATAAACAGAAAGGAGCTTTTGTATATAATCATATGATCGACTGCTTTGATTCAGGCT 840
Qy 880 GTTCAAGGTGAAGATTCATGAGTCTATATAAAGGCTTTTACCATCTTGGCTGAGAAATG 939
Db 841 GTTCAAGGTGAAGATTCATGAGTCTATATAAAGGCTTTTACCATCTTGGCTGAGAAATG 900
Qy 940 ACCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGATGAGTGGAGTC 999
Db 901 ACCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGATGAGTGGAGTC 960
Qy 1000 AGTCCATTTTAA 1011
Db 961 AGTCCATTTTAA 972

RESULT 8
AB106930
LOCUS Mus musculus UCP4 mRNA for uncoupling protein 4, complete cds.
DEFINITION AB106930
ACCESSION AB106930
VERSION AB106930.1 GI:29365510
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Hitomi,Y., Moriya,S., Matsushita,K. and Tanaka,H.
TITLE Molecular cloning of mouse UCP4 cDNA
JOURNAL Unpublished
REFERENCE 2
AUTHORS Hitomi,Y., Moriya,S., Matsushita,K. and Tanaka,H.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-2003) Yoshinori Hitomi, Utsunomiya University, Faculty of Agriculture, 350 Mine-machi, Utsunomiya, Tochigi 321-8505, Japan (E-mail:hitomik@cc.utsunomiya-u.ac.jp, Tel:81-28-649-5465, Fax:81-28-649-5401)

FEATURES
source
1..2851
/organism="Mus musculus"
/mol_type="mRNA"
/strain="ICR"
/db_xref="taxon:10090"
/sex="female"
/tissue_type="brain"
1..2851
/genes="UCP4"
158..1126
/genes="UCP4"
/codon_start=1
/product="uncoupling protein 4"
/protein_id="BAC66453.1"
/db_xref="GI:29365511"
/translation="MPIAEBEKLLPLTORWPRTSKFLGSCAATVAELATFPLDLTKT
RLMQCEAALALRGDGVAPYRGVMVRTALGIVQEGFLKMQGVTPAIRYRVVYSG
GRNVYEHLERVVFGSEKDYPLWKSIVGGMWAGVIGFLANPDLVKVQMEGR
RLGKPLRFGRVHFAFKLAEGLRGLWAGIPNIQRAALVNMGLDITVTKHLYL
LNPDLNISTSLCSGLVASILGTPADVIKSRIMNPRDKQGRGLLYKSSADCL
IQAVQEGFLSLYKGLPLPSWLRTPWSMVFWLTLYEKIREMSGVSPF"
```

```
ORIGIN
Query Match 76.3%; Score 793; DB 10; Length 2851;
Best Local Similarity 89.1%; Pred. No. 2.2e-216;
Matches 854; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
Qy 55 GAGGAGGAGAGGCTTTTGGCGCTGACCCAGAGATGGCCCGAGCGAGCAAAATTCCTACTG 114
Db 170 GAGGAGGAGAGGCTGTGCGCTCAACGAGAGATGGCCCGAGCGAGCAAAATTCCTACTG 229
Qy 115 TCCGGCTGCGCGCTACCGTGGCGGAGCTAGCAACCTTTCCCTCGATCTCACAANAATCT 174
Db 230 TCCGGCTGCGCGCAACCGTGGCGGAGCTAGCAACCTTTCCCTCGATCTCACAANAATCT 289
Qy 175 CGACTCCAAATGCAAGAGAGAGAGCTCTTGTCTCGTGGGAGACGGTGAAGAGAAATCT 234
Db 290 CGACTCCAGATGCAAGAGAGAGCTGCCCTTGTCTAGGTTGGAGATGGCGGAGTGGACTCT 349
Qy 235 GCCCCTTATAGGGGAATGGTGGCGACAGCCCTAGGGATCATTTGAAGAGGAAGGCTTTCTA 294
Db 350 GCCCCTTATAGGGGATGGTGGCGACAGCCCTGGGAATGTTTCAGGAGGAAGGCTTCTTA 409
Qy 295 AAGCTTTGGCAAGGAGTGAACCCGCCATTTACAGACAGTAGTGTATTTCTGAGGTGCA 354
Db 410 AAGCTGTGGCAAGGAGTGAACCCGCCATTTACAGACAGTAGTGTATTTCTGAGGTGCG 469
Qy 355 ATGGTCAATATGAACATCTCCGAGAGGTTGTCTTTGGCAAAAGTGAAGATGAGCATTAT 414
Db 470 ATGGTCACTATGAACATCTACGGGAAGTGTCTTTGGCAAAAGTGAAGATGAGCATTAT 529
Qy 415 CCCCTTTGAAATCAGTCAATTTGAGGGATGATGGCTGGTGTATTATGGCCAGTTTATAGCC 474
Db 530 CCCCTCTGAAATCGGTCAATTTGAGGGATGATGGCTGGTGTATCTCGACAGTTTATAGCC 589
Qy 475 AATCCAACTGACCTAGTGAAGTTTCAAGTGCATAATCGAAGGAAAAAGGAAACTGGAAGGA 534
Db 590 AATCCCACTGACCTTGTGAAGTCCAGATGCAAAATGGAAGGAAAAAGGAACTGGAAGGG 649
Qy 535 AAACCAATTCGATTTTCGTGTGTACATCATGATTTTGCATAAATCTTAGCTGAAGGAGGA 594
Db 650 AAACCTTTGAGATTCCGTGGAGTACATCATGATTTTGCATAAATCTTAGCTGAAGGAGGA 709
Qy 595 ATACGAGGGCTTTGGCGAGGCTGGGTACCCAATATATCAAAAGACAGCAGTGGTGAATATG 654
Db 710 ATCCGCGGGCTTTGGCGAGGCTGGAATACCAATATTTACAGAGACAGCGCTTGTGAACATG 769
Qy 655 GAGATTTTAAACCACTTATGATACAGTGAACACTACTTGGTATTGAATACACCACTTGAG 714
Db 770 GAGATCTTAAACCACTTACGACACAGTGAACACTACTTGGTATTGAACACACCGCTTGAA 829
Qy 715 GACAATATCATGACTCACCGTTTATCAAGTTTATGTTCTGGACTGGTGGTCTTCTATTCTG 774
Db 830 GACAATATTTCCACCCAGGCTTATCCAGTTTGTGTCTGGACTTGTGGCTTCTATTCTG 889
Qy 775 GGAACACCAAGCCGATGTCTCAAAAAGCAGAAATAATGAATCAACACAGAGATAAACCAAGGA 834
Db 890 GGAACACCAAGCCGATGTCTCAAAAAGCCGAATAATGAACCACTCGAGACAAACCAAGGA 949
Qy 835 AGGGGACTTTTGTATATAATCATGACTGATGCTGCTGATTTAGGCTGTTTCAAGGTGAAGGA 894
Db 950 AGGGGACTTTTGTATATAAGTTCATGAGCTGATGCTGCTGATCCAGGCTGTTCAGGGGAGGC 1009
Qy 895 TTCATGAGTCTATATAAAGGCTTTTACCATCTTGGCTGAGAGATGACCCCTTCGTCAATG 954
Db 1010 TTCCTGAGCTGTATATAAGGCTTTTACCCCTCGTGGCTGAGAGATGAGTGGAGTCAAGT 1069
Qy 955 GTGTTCTGGCTTACTTTATGAAAAAATCAGAGAGATGAGTGGAGTCAAGTTCATTTTAAAG 1012
Db 1070 GTGTTCTGGCTCCTTATGAAAAAATCCCGAGAGATGAGTGGAGTCAAGTTCATTTTAAAG 1127

RESULT 9
RNO300162
```

LOCUS RNO300162 2678 bp mRNA linear ROD 06-JAN-2001
 DEFINITION Rattus norvegicus mRNA for uncoupling protein UCP-4 (Ucp-4 gene), isoform a.
 ACCESSION AJ300162
 VERSION AJ300162.1 GI:12055539
 KEYWORDS isoform a; Ucp-4 gene; Uncoupling protein UCP-4.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1 Alberati-Giani, D., Gatti, S., Rial, E., Danel, F., Hauser, N., Bubendorff, C. and Bartfai, T.
 TITLE Three different isoforms of UCP-4 are expressed in rat preoptic anterior hypothalamus
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2678)
 AUTHORS Alberati-Giani, D.
 TITLE Direct Submission
 JOURNAL Submitted (02-NOV-2000) Alberati-Giani D., Pharma Division
 Preclinical Research, CNS, F. Hoffmann-La Roche Ltd., Grenzacherstrasse 124, CH 4070 Basel, SWITZERLAND
 FEATURES
 Location/Qualifiers
 1..2678
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague Dawley"
 /db_xref="taxon:10116"
 /sex="male"
 /tissue_type="brain, preoptic anterior hypothalamus"
 /dev_stage="6 weeks"
 /tissue_lib="UNI-ZAP custom cDNA library"
 /country="Switzerland"
 1..2678
 /gene="Ucp-4"
 52..1020
 /gene="Ucp-4"
 /function="uncouples respiration in eukaryotic cells"
 /codon_start=1
 /product="uncoupling protein UCP-4, isoform a"
 /protein_id="CAC20898.1"
 /db_xref="GI:12055540"
 /db_xref="GOA:Q9EPH7"
 /db_xref="SPRMBL:Q9EPH7"
 /translation="MPPPEESLQPLTQWRPRTSKFLSGCAATVAELATFPLDLTKT
 RLQMQEALAKLGDGMESAPYRGMRTALGIVQSEGLKMQGTPALYRHVYVSG
 GRWVTEHLREVYFGSEDEHYELWKSIVGGMWAGVIGQFLANPTDLVKVQMQEGR
 RLQKPLFRGVHFAKILAEGLRGLWAGWIPNTQRAALVNMGLTDTYDVYKHLV
 LNTALEDNIAHGLSLCSGLVASILGTPADVIKSRIMNPQRDKQGRGLLYKSTDCV
 IQAVQEGFLSLYKGLPLSLWRLTPMSVFWLTYEKIRQLSGVSPF"
 ORIGIN
 Query Match 75.6%; Score 785; DB 10; Length 2678;
 Best local similarity 87.6%; Pred. No. 4.3e-214;
 Matches 870; Conservative 0; Mismatches 120; Indels 3; Gaps 1;
 QY 20 TCGTCTTCCGCTACTGCTGAATGTCGTCGCCGAGGAGGAGAGGCTTTTCGCCGCTGA 79
 DB 32 TGGTCTGACCTGCTGCTGAATGCTTTTCCC---TGAGGAGGAGTGCCTACAGCCACTCA 88
 QY 80 CCAGAGATGCCCGGAGCGAGCAAAATTCCTACTGTCCGCTCGCGGCTACCGTGGCCG 139
 DB 89 CGCAGAGATGCCCGGAGCGAGCAAGTTCCTACTGTCCGCTCGCGGCAACCGTGGCCG 148
 QY 140 AGCTAGCAACTTTCCTCCGCTGATCTCACAAAATCTGATCCCAATTCAGGAGAGAGCAG 199
 DB 149 AGCTAGCAACTTTCCTCCGCTGATCTCACAAAATCCGACTCCAGATGCAAGGAGAGCTG 208
 QY 200 CTCCTGCTGGTGGAGAGCGGTGCAAGAGAAATCTGCCCTATAGGGAATCGTGGCGCA 259
 DB 209 CCCTTGCTAAGTTGGGAGATGGTGGCAGTGAATCCGCCCTTACAGGGGCATGATCGCA 268

QY 260 CAGCCCTAGGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTGGCAAGGAGTGCACCCG 319
 DB 269 CGGCCCTGGGATGTGTCAGGAGGAGGCTTCTAAAGTTGTGCAAGGAGTGCACCCG 328
 QY 320 CCATTTACAGACACGTAGTGTATTCTGGAGGTGCAATGGTGCATATGAACATCTCCGAG 379
 DB 329 CCATTTACAGACACGTAGTGTACTCTGGAGGTGGATGGTGCATCTAGCAACATCTCCGG 388
 QY 380 AGTTGTGTTGGCAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 439
 DB 389 AAGTTGTGTTGGCAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 448
 QY 440 GGATGATGGCTGCTGTATTGGCCAGTCTTTAGCCCAATCCAACTGACCTAGTGAAGTTC 499
 DB 449 GGATGATGGCTGCTGCTCATCGGACAGTCTTTAGCCCAATCCAACTGACCTAGTGAAGTTC 508
 QY 500 AGATGCAAAATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 559
 DB 509 AGATGCAAAATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 568
 QY 560 ATCATGCAATTTGCAAAATCTTTAGCTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 619
 DB 569 ATCATGCAATTTGCAAAATCTTTAGCTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 628
 QY 620 TACCCCAATATACAAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 679
 DB 629 TACCCCAATATATACAAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 688
 QY 680 TGAACCACTACTTGGTATTGAATACACCACTTTGAGGAGCAATATCATGACTCAGCGTTAT 739
 DB 689 TGAACCACTACTTGGTATTGAATACACCACTTTGAGGAGCAATATCATGACTCAGCGTTAT 748
 QY 740 CAAGTTTATGTTCTGCACTGGTACTTCTATTCTGGGAAACACGAGCGGATGTCATCAAAA 799
 DB 749 CCAGTTTGTGTTCTGCACTGGTACTTCTATTCTGGGAAACACGAGCGGATGTCATCAAAA 808
 QY 800 GCAGAATAATGAATCAACACGAGAGATAAACAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 859
 DB 809 GCGAATAATGAATCAACACGAGAGATAAACAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 868
 QY 860 CTGACTGCTGATTCAGGCTGTTTCAAGGTGAAGGATTCATGAGTCTATATAAGGCTTTT 919
 DB 869 CTGACTGCTGATTCAGGCTGTTTCAAGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 928
 QY 920 TACCACTTCTGGCTGAGAATGACCCCTTGTCTCAATGCTGCTGCTGCTGCTGCTGCTGCTG 979
 DB 929 TACCCCTCTGGCTGAGAATGACCCCTTGTCTCAATGCTGCTGCTGCTGCTGCTGCTGCTG 988
 QY 980 TCAGAGAGATGATGGAGTCAAGTCCATTTTAAAG 1012
 DB 989 TCAGAGAGATGATGGAGTCAAGTCCATTTTAAAG 1021
 RESULT 10
 LOCUS BC033091
 DEFINITION Homo sapiens soluble carrier family 25, member 27, mRNA (cDNA clone MGC:45657 IMAGE:5455903), complete cds.
 ACCESSION BC033091
 VERSION BC033091.1 GI:21620095
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1339)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uscdin, T.B., Toshiyuki, S.,

gene
CDS
/sex="male"
/tissue type="brain, preoptic anterior hypothalamus"
/dev stage="6 weeks"
/tissue lib="UNI-ZAP custom cDNA library"
/country="Switzerland"
1. .2620
/gene="Ucp-4"
139. .1173
/gene="Ucp-4"
/function="uncouples respiration in eukaryotic cells"
/codon start=1
/product="uncoupling protein UCP-4, isoform b"
/protein id="CAC20899.1"
/db_xref="GI:1205542"
/db_xref="GOA:Q9EPH6"
/db_xref="SPTREMBL:Q9EPH6"
/translation="MRPPEESLOPLTORWPRTSKELLSGCAATVAELATFPLDLTKT
RLQMGEEALAKLGDGMSAPRGMRTALGIVBEEGFLKLWQGVTPALYRHRVTS
GRMVTYHREVVFGKSEDEHYPLKWSVIGMGWVIGQFLANFTDLVQVQMEGR
RLEGKPLRFRGVHAFKILAEGLRGLWAGWIPNIOAALVNMGLDLYTDVYKHLV
LNTALEDNIALTHGLSLCSGLVASILGTADVKSRIMNQPRDKQGRGLYKSSYDCV
IOAVQGEGLSLYKGLPLPSLWRMEDTLHHRDCDLQGLATLYPSLETGVLSDSYFLRAI
CLVQSHETHN"

ORIGIN
Query Match 68.8%; Score 715.2; DB 10; Length 2620;
Best Local Similarity 86.8%; Pred. No. 5e-194;
Matches 799; Conservative 0; Mismatches 118; Indels 3; Gaps 1;

QY 20 TCGTCTTGGCGTACTGCTGAATCTCGTCCCGGAGGAGGAGAGCGCTTTTGGCCGCTGA 79
DB 119 TGGTCTGACCTGCTGCTGAATGCCCTTTTCCC---TGAGGAGGAGTCCGTACAGCCACTCA 175
QY 80 CCCAGAGATGGCCCGGAGGAGCAATCTCTACTGTCGCGCTCCGCGCTACCGTGGCGG 139
DB 176 CGCAGAGATGGCCCGGAGGAGCAATCTCTACTGTCGCGCTCCGCGCTACCGTGGCGG 235
QY 140 AGCTAGCAACCTTTTCCCTCGATCTCAAAAACTCGACTCCAAATGCAAGGAGAGAGCAG 199
DB 236 AGCTAGCAACCTTTTCCCTCGATCTCAAAAACTCGACTCCAAATGCAAGGAGAGCAG 295
QY 200 CTCTTCTCGTTGGGAGAGCGTGCAGAGAAATCTGCCCTTATAGGGAATGGTCCGGA 259
DB 296 CCCTTCTAAGTTGGGAGATGGTGCATGGAATCCGCCCTTACAGGGGCGATGATCGGA 355
QY 260 CAGCCCTAGGATCATGAGAGAGAGGCTTTCTAAGCTTTGGCAAGGAGTGACACCCG 319
DB 356 CGGCCCTGGGATTTGTCAGAGGAGAGGCTTCTTAAAGTTGTGGCAAGGAGTGACGCCG 415
QY 320 CCATTTACAGACAGTAGTGATTTCTGGAGGTGCAATGGTGCATATGAACATCTCCGAG 379
DB 416 CCATTTACAGACAGTAGTGATTTCTGGAGGTGCGATGGTGCATATGAACATCTCCGAG 475
QY 380 AGTTCTGTTTGGCAAAAGTGAAGATGAGCATTTATCCCTTTTGGAAATCAGTCAATGGAG 439
DB 476 AAGTTGTTTGGCAAAAGTGAAGATGAGCATTTATCCCTCTCGAAGTCCGTCAATGGAG 535
QY 440 GGATGATGGTGTGTTATTTGGCCAGTTTATAGCCCATCCAACTGACCTAGTGAAGGTT 499
DB 536 GGATGATGGTGTGTTATTTGGCCAGTTTATAGCCCATCCAACTGACCTAGTGAAGGTT 595
QY 500 AGATGCAATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 559
DB 596 AGATGCAATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 655
QY 560 ATCATGCAATTTGCAAAATCTTAGCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 619
DB 656 ATCATGCAATTTGCAAAATCTTAGCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 715
QY 620 TACCCCAATATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 679
DB 716 TACCCCAATATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 775

QY 680 TGAACACATCTTGGTATTGAATACACCACTTGGAGGAGCAATATCATGACTCAGCGTTTAT 739
DB 776 TGAAGCACTACCTGGTATTGAACACACAGCACTTGAAGACAATATCGCACTCAGCGTTAT 835
QY 740 CAAGTTTATGTTCTGCACTGGTGTCTTCTTCTGGGAGACACAGCGGATGTCTATCAAAA 799
DB 836 CCAGTTTGTGTTCTGGACTGGTGGCTTCTTCTTCTGGGAGACACAGCGGATGTCTATCAAAA 895
QY 800 GCAGATAATGAATCAACCAACGAGATATAACAAGGAGGAGGAGGAGGAGGAGGAGGAGG 859
DB 896 GCCGATAATGAACCAACCTCGAGACAAACAGGAGAGGAGGAGGAGGAGGAGGAGGAGG 955
QY 860 CTGACTGCTTGAATCAAGCTGTTCAGGTGAAGGATTCATGAGTCTATATATAAGGCTTTT 919
DB 956 CTGACTGCTGATCAGGCTGTTCAGGAGAGGAGGCTTCTGAGGCTGTATATAAGGCTTTC 1015
QY 920 TACCCTTCTGGCTGAGATG 939
DB 1016 TACCCTTCTGGCTGAGATG 1035
RESULT 13
AX061217
LOCUS AX061217 1726 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 64 from Patent WO0078953.
ACCESSION AX061217
VERSION AX061217.1 GI:12406353
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Lal, P., Yang, J., Yue, H., Hillman, J. L., Tang, Y. T., Bandman, O.,
Burford, N., Baughn, M. R., Azimzai, Y., Lu, D. A., Au-Young, J. and
Patterson, C.
TITLE Human transport proteins
JOURNAL Patent: WO 0078953-A 64 28-DEC-2000;
Incyte Genomics, Inc. (US)
FEATURES
source
1..1726
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 65.1%; Score 676.8; DB 6; Length 1726;
Best Local Similarity 99.7%; Pred. No. 5.3e-183;
Matches 678; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 332 ACGTAGTGATTTCTGGAGGTGCAATGGTGCATATCAATCAATCTCCGAGAGGTTGTGTTG 391
DB 452 ACCAGTGATTTCTGGAGGTGCAATGGTGCATATCAATCAATCTCCGAGAGGTTGTGTTG 511
QY 392 GCAAAAGTGAAGATGAGCATTTATCCCTTTTGGAAATCAGTCAATTGGAGGATGATGCTG 451
DB 512 GCAAAAGTGAAGATGAGCATTTATCCCTTTTGGAAATCAGTCAATTGGAGGATGATGCTG 571
QY 452 GTGTTATGGCCGTTTATAGCCATCCAACTGACCTAGTGAAGGTTTCAGATCAATGAG 511
DB 572 GTGTTATGGCCGTTTATAGCCATCCAACTGACCTAGTGAAGGTTTCAGATCAATGAG 631
QY 512 AAGGAAAAAGGAACTGGGAAGGAAACCATTTGGGATTTCTGTTGTGTACATCATGCAATTG 571
DB 632 AAGGAAAAAGGAACTGGGAAGGAAACCATTTGGGATTTCTGTTGTGTACATCATGCAATTG 691
QY 572 CAAAAATCTTAGCTGAAGGAGGAAATACGAGGCGCTTTGGGAGGCTGGGTACCCCAATATAC 631
DB 692 CAAAAATCTTAGCTGAAGGAGGAAATACGAGGCGCTTTGGGAGGCTGGGTACCCCAATATAC 751
QY 632 AAAGAGCAGACTGGTGAATATAGGAGATTTAAACCACTTATGATACAGTGAACACTACT 691
DB 752 AAAGAGCAGACTGGTGAATATAGGAGATTTAAACCACTTATGATACAGTGAACACTACT 811

```

QY 692 TGGTATTGAATACACCACTTGGAGCAATATCATGACTCAGGTTTATCAAGTTTATGTT 751
Db 812 TGGTATTGAATACACCACTTGGAGCAATATCATGACTCAGGTTTATCAAGTTTATGTT 871
QY 752 CTGGACTGGTAGCTTCTATTCTGGGAACACAGCCGATGTCATCAAAAGCAGAAATATGA 811
Db 872 CTGGACTGGTAGCTTCTATTCTGGGAACACAGCCGATGTCATCAAAAGCAGAAATATGA 931
QY 812 ATCAACACAGAGATAAACAAGGAAGGGAGCTTTTGTATATAATCATCGACTGCTTGA 871
Db 932 ATCAACACAGAGATAAACAAGGAAGGGAGCTTTTGTATATAATCATCGACTGCTTGA 991
QY 872 TTCAAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAGGCTTTTACCCTCTTGGC 931
Db 992 TTCAAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAGGCTTTTACCCTCTTGGC 1051
QY 932 TGAGAAATGACCCCTTGGTCAATGTTCTTGGCTTACTTATGAAAAAATCAGAGAGATGA 991
Db 1052 TGAGAAATGACCCCTTGGTCAATGTTCTTGGCTTACTTATGAAAAAATCAGAGAGATGA 1111
QY 992 GTGGAGTCAGTCCATTAA 1011
Db 1112 GTGGAGTCAGTCCATTAA 1131

RESULT 14
AX746657 3266 bp mRNA linear PAT 20-JUN-2003
LOCUS
DEFINITION Sequence 182 from Patent EP1308459.
ACCESSION AX746657
VERSION AX746657.1 GI:32130924
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Isegai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.
TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1308459-A 182 07-MAY-2003;
Helix Research Institute (JP) ; Research Association for
Biotechnology (JP)
FEATURES
source Location/Qualifiers
1 .3266
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 65.1%; Score 676.8; DB 6; Length 3266;
Best Local Similarity 99.7%; Pred. No. 5.6e-183;
Matches 678; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 332 ACCTAGTGTATTCGGAGGTCGAATGTCATATGAATCAATCCCGAGAGGTTGTGTTG 391
Db 900 ACCCAGTGTATTCGGAGGTCGAATGTCATATGAATCAATCCCGAGAGGTTGTGTTG 959
QY 392 GCAAACTGGAAGTACATATTCCTTTGGAAATCAGTCATTTGGAGGATCATGCTG 451
Db 960 GCAAACTGGAAGTACATATTCCTTTGGAAATCAGTCATTTGGAGGATCATGCTG 1019
QY 452 GTGTTATTGGCCAGTTTTAGCCAAATCCAACTGACCTAGTGAAGGTTTCAGATCAATGG 511
Db 1020 GTGTTATTGGCCAGTTTTAGCCAAATCCAACTGACCTAGTGAAGGTTTCAGATCAATGG 1079
QY 512 AAGAAAAAGAACTGGGAAGGAAACCATTTGGATTTCTGGTGTACATCATGCTTTG 571
Db 1080 AAGAAAAAGAACTGGGAAGGAAACCATTTGGATTTCTGGTGTACATCATGCTTTG 1139

```

```

QY 572 CAAAAATCTTAGCTGAAGGAGGAATACGAGGCTTTGGGCGAGCTGGGTACCCAAATATAC 631
Db 1140 CAAAAATCTTAGCTGAAGGAGGAATACGAGGCTTTGGGCGAGCTGGGTACCCAAATATAC 1199
QY 632 AAAGAGCAGCACTGGTGAATATCGGAGATTAAACCACTTATGATACAGTGAACACTACT 691
Db 1200 AAAGAGCAGCACTGGTGAATATCGGAGATTAAACCACTTATGATACAGTGAACACTACT 1259
QY 692 TGGTATTGAATACACCACTTGGAGCAATATCATGACTCAGGTTTATCAAGTTTATGTT 751
Db 1260 TGGTATTGAATACACCACTTGGAGCAATATCATGACTCAGGTTTATCAAGTTTATGTT 1319
QY 752 CTGGACTGGTAGCTTCTATTCTGGGAACACAGCCGATGTCATCAAAAGCAGAAATATGA 811
Db 1320 CTGGACTGGTAGCTTCTATTCTGGGAACACAGCCGATGTCATCAAAAGCAGAAATATGA 1379
QY 812 ATCAACACAGAGATAAACAAGGAAGGGAGCTTTTGTATATAATCATCGACTGCTTGA 871
Db 1380 ATCAACACAGAGATAAACAAGGAAGGGAGCTTTTGTATATAATCATCGACTGCTTGA 1439
QY 872 TTCAAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAGGCTTTTACCCTCTTGGC 931
Db 1440 TTCAAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAGGCTTTTACCCTCTTGGC 1499
QY 932 TGAGAAATGACCCCTTGGTCAATGTTCTTGGCTTACTTATGAAAAAATCAGAGAGATGA 991
Db 1500 TGAGAAATGACCCCTTGGTCAATGTTCTTGGCTTACTTATGAAAAAATCAGAGAGATGA 1559
QY 992 GTGGAGTCAGTCCATTAA 1011
Db 1560 GTGGAGTCAGTCCATTAA 1579

RESULT 15
AK090871 3266 bp mRNA linear PRI 15-JUL-2002
LOCUS
DEFINITION Homo sapiens cDNA FLJ33552 fis, clone BRAMY2009123, highly similar
to MITOCHONDRIAL UNCOUPLING PROTEIN 4.
ACCESSION AK090871.1 GI:21749113
VERSION
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 Tashiro,H., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S.,
Fukuzumi,Y., Fujimori,Y., Komiya,M., Sugiyama,T., Irie,R.,
Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isegai,T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 3266)
Isegai,T. and Yamamoto,J.
Direct Submission
Submitted (04-JUL-2002) Takao Isegai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
Location/Qualifiers
1 .3266
/organism="Homo sapiens"

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRAMY2009123"
/tissue_type="amygdala"
/clone_lib="BRAMY2"
/note="Cloning vector: pME18SFL3"

ORIGIN

```
Query Match      65.1%; Score 676.8; DB 9; Length 3266;
Best Local Similarity 99.7%; Pred. No. 5.6e-183;
Matches 678; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 332 ACCTAGTGTATTCGAGGTCGAATGGTCAATATGAACATCTCCGAGAGGTTGTGTTG 391
Db 900 ACCCAGTGTATTCGAGGTCGAATGGTCAATATGAACATCTCCGAGAGGTTGTGTTG 959

QY 392 GCAAAAGTGAAGATGAGCATTTCCCTTTGGAAATCAGTCATTGGAGGATGATGCTG 451
Db 960 GCAAAAGTGAAGATGAGCATTTCCCTTTGGAAATCAGTCATTGGAGGATGATGCTG 1019

QY 452 GTGTTATTGGCCAGTTTTTACCCAATCCAACTGACCTAGTGAAGGTTTCAGATGCAAAATGG 511
Db 1020 GTGTTATTGGCCAGTTTTTACCCAATCCAACTGACCTAGTGAAGGTTTCAGATGCAAAATGG 1079

QY 512 AAGGAAAAGGAACTCGGAAGGAAACCAATGCGATTTCTGTGTGATCATCATGCAATTTG 571
Db 1080 AAGGAAAAGGAACTCGGAAGGAAACCAATGCGATTTCTGTGTGATCATCATGCAATTTG 1139

QY 572 CAAAATCTTAGCTGAGGAGGAATACGAGGCTTTGGGAGGCTGGGTACCCCAATATAC 631
Db 1140 CAAAATCTTAGCTGAGGAGGAATACGAGGCTTTGGGAGGCTGGGTACCCCAATATAC 1199

QY 632 AAAGAGCAGCAGTGTGAATATGGGAGATTAAACCCTTATGATACAGTGAAACACTACT 691
Db 1200 AAAGAGCAGCAGTGTGAATATGGGAGATTAAACCCTTATGATACAGTGAAACACTACT 1259

QY 692 TGGTATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTTATCAAGTTTATGTT 751
Db 1260 TGGTATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTTATCAAGTTTATGTT 1319

QY 752 CTGGACTGGTAGCTTCTATTCTGGGAACACCGCCGATGTCATCAAAAGCAGAAATATGA 811
Db 1320 CTGGACTGGTAGCTTCTATTCTGGGAACACCGCCGATGTCATCAAAAGCAGAAATATGA 1379

QY 812 ATCAACCACGAGATAAACAGGAAGGGACTTTTGTATTAATCATCGACTGCTGCTTGA 871
Db 1380 ATCAACCACGAGATAAACAGGAAGGGACTTTTGTATTAATCATCGACTGCTGCTTGA 1439

QY 872 TTCAGGCTGTTCAGGTGAAGGATTTCATGAGTCTATATAAGGCTTTTACCATCTTGGC 931
Db 1440 TTCAGGCTGTTCAGGTGAAGGATTTCATGAGTCTATATAAGGCTTTTACCATCTTGGC 1499

QY 932 TGAGAAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGATGA 991
Db 1500 TGAGAAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGATGA 1559

QY 992 GTGGACTCAGTCCATTTTAA 1011
Db 1560 GTGGACTCAGTCCATTTTAA 1579
```

Search completed: September 24, 2004, 05:44:36
Job time : 4104 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2004, 03:57:38 ; Search time 453 Seconds

(without alignments)
9743.660 Million cell updates/sec

Title: US-09-397-342C-2

Perfect score: 1039

Sequence: 1 ccgagctcgatcccggttat.....cagatatcatcacactggc 1039

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001Bs:*

6: Geneseqn2002s:*

7: Geneseqn2003as:*

8: Geneseqn2003Bs:*

9: Geneseqn2003Cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1039	100.0	1039	3	AA14084 cDNA enco
2	998	96.1	998	3	AA14084 Human UCP
3	998	96.1	998	4	AA14084 Primer #1
4	998	96.1	998	4	AA14084 Human PRO
5	998	96.1	998	6	AB574440 Human CDN
6	998	96.1	998	7	ACA91226 Novel hum
7	998	96.1	998	7	ACD81603 Human CDN
8	998	96.1	998	7	ACA0425 Novel hum
9	998	96.1	998	7	ACA58872 cDNA enco
10	998	96.1	998	7	ACA64048 cDNA enco
11	998	96.1	998	7	ACA91312 cDNA enco
12	998	96.1	998	7	ACD45211 Human sec
13	998	96.1	998	7	ACA93759 Human CDN
14	998	96.1	998	7	ACA67333 cDNA enco
15	998	96.1	998	7	ACH66306 Novel hum
16	998	96.1	998	7	ACD02360 Novel hum
17	998	96.1	998	7	ACA89351 Novel hum
18	998	96.1	998	7	ACA68988 Novel hum
19	998	96.1	998	7	ACA98510 Human PRO
20	998	96.1	998	7	ACA63435 cDNA enco
21	998	96.1	998	8	ADB17182 Human CDN
22	998	96.1	998	8	ACH03638 Human sec
23	998	96.1	998	8	ACD68526 Novel hum

ALIGNMENTS

RESULT 1
AA14084
ID AA14084 standard; cDNA; 1039 BP.
XX
AC AA14084;
XX
DT 21-JUL-2000 (first entry)
XX
DE cDNA encoding human uncoupling protein UCP4.

XX
KW Uncoupling protein; UCP4; expressed sequence tag; EST; human;
KW Chromosome 6p11.2-q12; ATP synthesis; energy efficiency;
KW Mitochondrial membrane; proton leakage; heat production; metabolic rate;
KW drug screening; obesity; stroke; trauma; sepsis; infection; ss.
XX Homo sapiens.

OS
FH Key
CDS
FT Location/Qualifiers
FT 40..1011
FT /*tag= a
FT /product= "Human UCP4"

XX WO200017353-A1.

XX 30-MAR-2000.

XX 15-SEP-1999; 99WO-US021194.

XX 22-SEP-1998; 98US-0101279P.

XX 30-DEC-1998; 98US-0114223P.

XX 16-APR-1999; 99US-0129674P.

XX (GETH) GENENTECH INC.

XX Adams S, Pan J, Zhong A;

XX WPI; 2000-292842/25.

XX P-PSDB; AAY81497.

XX New nucleic acid encoding human uncoupled protein-4, useful e.g for
XX identifying metabolic regulators for treatment of obesity.

XX Claim 3; Fig 2; 80pp; English.

XX This sequence represents cDNA encoding human uncoupling protein UCP4. The
XX human UCP4 cDNA (ATCC 203134) was isolated from a brain cDNA library

PR	15-SEP-1998;	98US-0100390P.	PR	29-OCT-1998;	98US-0106248P.	XX	(GETH) GENENTECH INC.
PR	16-SEP-1998;	98US-0100584P.	PR	29-OCT-1998;	98US-0106384P.	XX	Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
PR	16-SEP-1998;	98US-0100627P.	PR	29-OCT-1998;	98US-0108500P.	XX	WPI: 2000-237871/20.
PR	16-SEP-1998;	98US-0100661P.	PR	30-OCT-1998;	98US-0106464P.	DR	P-PSDB; AAY99457.
PR	16-SEP-1998;	98US-0100662P.	PR	30-OCT-1998;	98US-0106856P.	DR	New mammalian DNA sequences encoding transmembrane, receptor or secreted
PR	16-SEP-1998;	98US-0100664P.	PR	30-OCT-1998;	98US-0106902P.	XX	PRO polypeptides, useful for screening of potential peptide or small
PR	17-SEP-1998;	98US-0100683P.	PR	03-NOV-1998;	98US-0108905P.	XX	molecule inhibitors of the relevant receptor/ligand interactions.
PR	17-SEP-1998;	98US-0100684P.	PR	03-NOV-1998;	98US-0108919P.	XX	Claim 2; Fig 235; 773pp; English.
PR	17-SEP-1998;	98US-0100710P.	PR	03-NOV-1998;	98US-0106932P.	XX	AAA37022 to AAA37144 encode the new isolated human transmembrane,
PR	17-SEP-1998;	98US-0100711P.	PR	03-NOV-1998;	98US-0106933P.	CC	receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
PR	17-SEP-1998;	98US-0100919P.	PR	03-NOV-1998;	98US-0107783P.	CC	transmembrane and receptor PRO proteins can be used for screening of
PR	17-SEP-1998;	98US-0100930P.	PR	17-NOV-1998;	98US-0108775P.	CC	potential peptide or small molecule inhibitors of the relevant
PR	18-SEP-1998;	98US-0100848P.	PR	17-NOV-1998;	98US-0108777P.	CC	receptor/ligand interactions. The polypeptides and nucleotide sequences
PR	18-SEP-1998;	98US-0100849P.	PR	17-NOV-1998;	98US-0108787P.	CC	encoding then have various industrial applications, including uses as
PR	18-SEP-1998;	98US-0101014P.	PR	17-NOV-1998;	98US-0108788P.	CC	pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
PR	18-SEP-1998;	98US-0101068P.	PR	17-NOV-1998;	98US-0108801P.	CC	primers and hybridisation probes used in the isolation of the PRO
PR	18-SEP-1998;	98US-0101071P.	PR	17-NOV-1998;	98US-0108802P.	XX	polypeptides from the present invention
PR	23-SEP-1998;	98US-0101279P.	PR	17-NOV-1998;	98US-0108806P.	XX	Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;
PR	23-SEP-1998;	98US-0101471P.	PR	17-NOV-1998;	98US-0108807P.	XX	Query Match 96.1%; Score 998; DB 3; Length 998;
PR	23-SEP-1998;	98US-0101472P.	PR	17-NOV-1998;	98US-0108867P.	XX	Best Local Similarity 100.0%; Pred. No. 0;
PR	23-SEP-1998;	98US-0101473P.	PR	17-NOV-1998;	98US-0108867P.	XX	Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PR	23-SEP-1998;	98US-0101474P.	PR	17-NOV-1998;	98US-0108867P.	XX	14 CCGTTATCGTCTTGCGCTACTGCTGAATGTCGTCCTCCGAGAGAGAGAGGCTTTTGC 73
PR	23-SEP-1998;	98US-0101475P.	PR	17-NOV-1998;	98US-0108849P.	XX	1 CCGTTATCGTCTTGCGCTACTGCTGAATGTCGTCCTCCGAGAGAGAGAGGCTTTTGC 60
PR	23-SEP-1998;	98US-0101476P.	PR	17-NOV-1998;	98US-0108849P.	XX	74 CGCTGACCCAGAGATGGCCCGAGGAGCAAAATTCCTACTCTCGGCTCGCGGCTACCG 133
PR	23-SEP-1998;	98US-0101477P.	PR	17-NOV-1998;	98US-0108850P.	XX	61 CGCTGACCCAGAGATGGCCCGAGGAGCAAAATTCCTACTCTCGGCTCGCGGCTACCG 120
PR	23-SEP-1998;	98US-0101479P.	PR	17-NOV-1998;	98US-0108851P.	XX	134 TGGCCGAGCTAGCAACCTTTTCCCTTGGATCTCACAAAAAATTCGACTCCAAATGCAAGGAG 193
PR	24-SEP-1998;	98US-0101738P.	PR	17-NOV-1998;	98US-0108852P.	XX	121 TGGCCGAGCTAGCAACCTTTTCCCTTGGATCTCACAAAAAATTCGACTCCAAATGCAAGGAG 180
PR	24-SEP-1998;	98US-0101741P.	PR	17-NOV-1998;	98US-0108853P.	XX	194 AAGCAGCTCTTGCTCGGTTGGAGACCGTGCAAGAGAAATTCGCCCCCTATAGGGGAATGG 253
PR	24-SEP-1998;	98US-0101743P.	PR	17-NOV-1998;	98US-0108854P.	XX	181 AAGCAGCTCTTGCTCGGTTGGAGACCGTGCAAGAGAAATTCGCCCCCTATAGGGGAATGG 240
PR	24-SEP-1998;	98US-0101915P.	PR	17-NOV-1998;	98US-0108855P.	XX	
PR	24-SEP-1998;	98US-0101916P.	PR	17-NOV-1998;	98US-0108904P.	XX	
PR	29-SEP-1998;	98US-0102207P.	PR	17-NOV-1998;	98US-0108904P.	XX	
PR	29-SEP-1998;	98US-0102240P.	PR	17-NOV-1998;	98US-0108904P.	XX	
PR	29-SEP-1998;	98US-0102307P.	PR	17-NOV-1998;	98US-0108925P.	XX	
PR	29-SEP-1998;	98US-0102330P.	PR	17-NOV-1998;	98US-0108948P.	XX	
PR	29-SEP-1998;	98US-0102331P.	PR	17-NOV-1998;	98US-0108948P.	XX	
PR	30-SEP-1998;	98US-0102484P.	PR	17-NOV-1998;	98US-0108948P.	XX	
PR	30-SEP-1998;	98US-0102487P.	PR				

QY	254	TGGCGACAGCCCTAGGGATCATTTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGA	313
DB	241	TGGCGCAGCCCTAGGGATCATTTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGA	300
QY	314	CACCCGCCATTTACACACACGCTAGTGTATTTCTGGAGGTCGAATGGTCACATATGAACATC	373
DB	301	CACCCGCCATTTACACACACGCTAGTGTATTTCTGGAGGTCGAATGGTCACATATGAACATC	360
QY	374	TCCGAGAGGTTGTGTTTGGCAAAAGTGAAGATGAGCATTTATCCCTTTTGGAAATCAGTCA	433
DB	361	TCCGAGAGGTTGTGTTTGGCAAAAGTGAAGATGAGCATTTATCCCTTTTGGAAATCAGTCA	420
QY	434	TTGGAGGGATGATGGCTGGTGTATTTAGGCCAGTTTTTTAGCCAAATCCAACTGACTAGTGA	493
DB	421	TTGGAGGGATGATGGCTGGTGTATTTAGGCCAGTTTTTTAGCCAAATCCAACTGACTAGTGA	480
QY	494	AGGTTTCAGATGCAATGGNAGGAAAGGAAACTGGGAAGGAAACCATTCGGATTTTCGTG	553
DB	481	AGGTTTCAGATGCAATGGNAGGAAAGGAAAGGAAACTGGGAAGGAAACCATTCGGATTTTCGTG	540
QY	554	GTGTACATCATGTTCGAAAAATCTTTAGCTGAAGGAGGAATAACGAGGCTTTTGGGCAG	613
DB	541	GTGTACATCATGTTCGAAAAATCTTTAGCTGAAGGAGGAATAACGAGGCTTTTGGGCAG	600
QY	614	GCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG	673
DB	601	GCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG	660
QY	674	ATACAGTGAACACACTACTTGGTATTGAATACACACTTTGAGGACAATATCATGACTCAGC	733
DB	661	ATACAGTGAACACACTACTTGGTATTGAATACACACTTTGAGGACAATATCATGACTCAGC	720
QY	734	GTTTATCAAGTTTATGTTCTCGACTGGTAGCTTCTATTCTGGGAACACAGCCGATGTCA	793
DB	721	GTTTATCAAGTTTATGTTCTCGACTGGTAGCTTCTATTCTGGGAACACAGCCGATGTCA	780
QY	794	TCAAAAGCAGATAATATGAATCAACACAGAGATAAACCAAGGAAGGGGACTTTTGTATAAAT	853
DB	781	TCAAAAGCAGATAATATGAATCAACACAGAGATAAACCAAGGAAGGGGACTTTTGTATAAAT	840
QY	854	CATCGACTGACTGCTTGATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTTATATAAAG	913
DB	841	CATCGACTGACTGCTTGATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTTATATAAAG	900
QY	914	GCTTTTTTACCATCTTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTCGCTTACTTATG	973
DB	901	GCTTTTTTACCATCTTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTCGCTTACTTATG	960
QY	974	AAAAAATCAGAGAGATGAGTGGAGTCAGTCCATTTTAA	1011
DB	961	AAAAAATCAGAGAGATGAGTGGAGTCAGTCCATTTTAA	998

PRECEDENT 3

RESULI 3
AAE54487

HAFF5448 /
TD 8858

AAFS
ID
YY

XX

AAFF
AC
yy

XX E

DT 02-1

XX 5

DE
Pri

XX:

KW
Secr

XX

OS
Unio

XX

PN WO20

XX

PD 28-1

XX

A-81 3d

XX	23-JUN-1999;	99US-0141037P.	
PR	20-JUL-1999;	99US-0144758P.	
PR	26-JUL-1999;	99US-0145698P.	
PR	01-SEP-1999;	99WO-US020111.	
PR	29-OCT-1999;	99US-0162508P.	
PR	30-NOV-1999;	99WO-US028313.	
PR	02-DEC-1999;	99WO-US028551.	
PR	16-DEC-1999;	99WO-US030095.	
PR	05-JAN-2000;	2000WO-US000219.	
PR	06-JAN-2000;	2000WO-US000376.	
XX			
PA	(GETH) GENENTECH INC.		
XX			
PI	Baker KP, Botstein D, Desnoyers L, Eaton DL, Fong S;		
PI	Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Hillan KJ;		
PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;		
PI	Williams PM, Wood WT;		
XX			
DR	WPI; 2001-071395/08.		
XX			
PT	Secreted and transmembrane proteins and nucleic acids designated PRO,		
PT	useful as hybridization probes, in chromosome and gene mapping and gene		
PT	therapy.		
XX			
PS	Example 120; Page 485; 787pp; English.		
XX			
CC	The present invention relates to secreted and transmembrane proteins.		
CC	These proteins and the DNA encoding them may be used as hybridization		
CC	probes, in chromosome and gene mapping and in the generation of anti-		
CC	sense RNA and DNA. They may also be used to generate either		
CC	transgenic animals or knockout animals which are in turn useful for		
CC	development and screening of therapeutically useful reagents. The nucleic		
CC	acids may also be used in gene therapy		
XX			
SQ	Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;		

4

QY 494 AGGTTGAGATGCAAAATGGAAGGAAAAAGGAACTGGAAGGAAACCAATGCGATTTTCGTG 553
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 481 AGGTTGAGATGCAAAATGGAAGGAAAAAGGAACTGGAAGGAAACCAATGCGATTTTCGTG 540
 QY 554 GTGTACATCATGCTATTTGCAAAATCTTAGCTGAAGGAGGAATACAGGGCTTTGGGCGAG 613
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 541 GTGTACATCATGCTATTTGCAAAATCTTAGCTGAAGGAGGAATACAGGGCTTTGGGCGAG 600
 QY 614 GCTGGGTGACCAATATACAAAGGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 673
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 601 GCTGGGTGACCAATATACAAAGGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 660
 QY 674 ATACAGTGAACACTCTTGGTATTTGAATACACCACTTGAGGACAATATCATGACTCACG 733
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 661 ATACAGTGAACACTCTTGGTATTTGAATACACCACTTGAGGACAATATCATGACTCACG 720
 QY 734 GTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAAACACGACCGGATGCA 793
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 721 GTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAAACACGACCGGATGCA 780
 QY 794 TCAAAAGCAGAATAATGAATCAACACGAGATAAACAAGGAGGAGACTTTTGTATAAAT 853
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 781 TCAAAAGCAGAATAATGAATCAACACGAGATAAACAAGGAGGAGACTTTTGTATAAAT 840
 QY 854 CATCGACTGACTGCTGATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAG 913
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 841 CATCGACTGACTGCTGATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAG 900
 QY 914 GCTTTTATCAATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTGCTTACTTATG 973
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 901 GCTTTTATCAATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTGCTTACTTATG 960
 QY 974 AAAAAATCAGAGAGATGAGTGGAGTCAAGTCCATTTTAA 1011
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 961 AAAAAATCAGAGAGATGAGTGGAGTCAAGTCCATTTTAA 998
 RESULT 4
 AAF92120
 ID AAF92120 standard; cdna; 998 BP.
 AC AAF92120;
 DX
 DT 15-MAY-2001 (first entry)
 XX
 XX Human PRO1566 cdna.
 XX Human; PRO protein; mapping; ss.
 KW Homo sapiens.
 OS
 PN WO200116318-A2.
 XX
 PD 08-MAR-2001.
 XX
 XX 24-AUG-2000; 2000WO-US023328.
 PF
 XX 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 07-DEC-1999; 99US-0169495P.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-JAN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 03-MAR-2000; 2000US-0170207P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 25-APR-2000; 2000US-0199397P.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 05-JUN-2000; 2000US-0209832P.
 XX

PA (GETH) GENENTECH INC.
 XX
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
 XX
 DR WPI; 2001-183260/18.
 DR P-PSDB; AAB87588.
 XX
 PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
 PT biology, including use as hybridization probes, and in chromosome and
 PT gene mapping.
 XX
 PS Claim 2; Fig 125; 278pp; English.
 XX
 CC The present sequence is the coding sequence for a human PRO polypeptide
 CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
 CC antagonists or anti-PRO antibodies are useful for preparation of a
 CC medicament useful in the treatment of a condition which is responsive to
 CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
 CC protein may also be employed as molecular weight markers for protein
 CC electrophoresis. The PRO coding sequence has applications in molecular
 CC biology, including use as hybridisation probes, and in chromosome and
 CC gene mapping
 XX
 SQ Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;
 Query Match 96.1%; Score 998; DB 4; Length 998;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 CGGTTATCGTCTTGGCTACTGCTGAATGTCCGTCGCGAGGAGGAGGAGGCTTTTGC 73
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1 CGGTTATCGTCTTGGCTACTGCTGAATGTCCGTCGCGAGGAGGAGGAGGCTTTTGC 60
 QY 74 CGCTGACCCAGAGATGCGCCCGAGCGAGCAAAATTCCTACTGTCGCGTCCGCGCTACCG 133
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 61 CGCTGACCCAGAGATGCGCCCGAGCGAGCAAAATTCCTACTGTCGCGTCCGCGCTACCG 120
 QY 134 TGGCCGAGCTAGCAACCTTTCCCTCGATCTCAGAAAACTCGACTCCAAATGCAAGGAG 193
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 121 TGGCCGAGCTAGCAACCTTTCCCTCGATCTCAGAAAACTCGACTCCAAATGCAAGGAG 180
 QY 194 AAGCAGCTCTTGTCTCGGTTGGGAGACGGTGCAGAGAAATCTGCCCTATAGGGGAATG 253
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 181 AAGCAGCTCTTGTCTCGGTTGGGAGACGGTGCAGAGAAATCTGCCCTATAGGGGAATG 240
 QY 254 TGGCGACAGCCCTAGGGATCATGAAGAGGAGGCTTTCTAAAGCTTTGCAAGGAGTGA 313
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 241 TGGCGACAGCCCTAGGGATCATGAAGAGGAGGCTTTCTAAAGCTTTGCAAGGAGTGA 300
 QY 314 CACCCGCCATTTACAGACACGTAGTGTATTTCTGGAGGTGAAATGTCACATATGAACATC 373
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 301 CACCCGCCATTTACAGACACGTAGTGTATTTCTGGAGGTGAAATGTCACATATGAACATC 360
 QY 374 TCCGAGAGGTGTGTGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAATTCAGTCA 433
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 361 TCCGAGAGGTGTGTGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAATTCAGTCA 420
 QY 434 TTGGAGGAGATGAGTGTGTGTTTATTTGGCCAGTTTTTAGCCAATCCAACTGAGCTAGTGA 493
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 421 TTGGAGGAGATGAGTGTGTGTTTATTTGGCCAGTTTTTAGCCAATCCAACTGAGCTAGTGA 480
 QY 494 AGGTTTCAGATGCAAAATGGAAGGAAAAAGGAACTGGAAGGAAAAACCAATTCGATTTTCGTG 553
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 481 AGGTTTCAGATGCAAAATGGAAGGAAAAAGGAACTGGAAGGAAAAACCAATTCGATTTTCGTG 540
 QY 554 GTGTACATCATGCTATTTGCAAAATCTTAGCTGAAGGAGGAATACAGGGCTTTGGGCGAG 613
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 541 GTGTACATCATGCTATTTGCAAAATCTTAGCTGAAGGAGGAATACAGGGCTTTGGGCGAG 600
 QY 614 GCTGGGTGACCAATATACAAAGGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 673
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 601 GCTGGGTGACCAATATACAAAGGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 660

QY 674 ATACAGTGAACACTACTTGGTATTGATATACACACTTGGAGCAATATCATGACTCAAG 733
 Db 661 ATACAGTGAACACTACTTGGTATTGATATACACACTTGGAGCAATATCATGACTCAAG 720
 QY 734 GTTTATCAAGTTTATGTTCTGGACTGGTGTCTTATCTGGGAACACACCGCGATGTCA 793
 Db 721 GTTTATCAAGTTTATGTTCTGGACTGGTGTCTTATCTGGGAACACACCGCGATGTCA 780
 QY 794 TCAAAACAGCAATATGAATCAACACAGAGATAAACCAAGGAAGGGGACTTTTGTATATAAT 853
 Db 781 TCAAAACAGCAATATGAATCAACACAGAGATAAACCAAGGAAGGGGACTTTTGTATATAAT 840
 QY 854 CATCGACTGACTGCTTCAATCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAG 913
 Db 841 CATCGACTGACTGCTTCAATCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAG 900
 QY 914 GCTTTTACCATCTTGGCTGAGATGACCCCTTGGTCAATGGTGTCTCTGGCTTACTTATG 973
 Db 901 GCTTTTACCATCTTGGCTGAGATGACCCCTTGGTCAATGGTGTCTCTGGCTTACTTATG 960
 QY 974 AAAAAATCAGAGATGAGTGGAGTCACTAGTCAATTTAA 1011
 Db 961 AAAAAATCAGAGATGAGTGGAGTCACTAGTCAATTTAA 998
 RESULT 5
 ABS74440
 ID ABS74440 standard; cdna; 998 BP.
 XX
 AC ABS74440;
 XX
 DT 10-DEC-2002 (first entry)
 XX
 DE Human cdna encoding secreted/transmembrane protein PRO1566.
 XX
 KW Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;
 KW antiarthritic; osteopathic; sports-related joint problem;
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US2002119130-A1.
 XX
 PD 29-AUG-2002.
 XX
 PF 06-DEC-2001; 2001US-00006867.
 XX
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 22-APR-1998; 98US-0082797P.
 PR 23-APR-1998; 98US-0083495P.
 PR 15-MAY-1998; 98US-0085579P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088030P.
 PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088740P.
 PR 10-JUN-1998; 98US-0088811P.
 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088825P.
 PR 11-JUN-1998; 98US-0088863P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 19-JUN-1998; 98US-0089952P.
 PR 22-JUN-1998; 98US-0090246P.
 PR 24-JUN-1998; 98US-0090444P.
 PR 25-JUN-1998; 98US-0090688P.
 PR 25-JUN-1998; 98US-0090696P.
 PR 26-JUN-1998; 98US-0090862P.
 PR 02-JUL-1998; 98US-0091628P.

PR 10-AUG-1998; 98US-0096012P.
 PR 17-AUG-1998; 98US-0096757P.
 PR 18-AUG-1998; 98US-0096949P.
 PR 18-AUG-1998; 98US-0096959P.
 PR 26-AUG-1998; 98US-0097954P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 26-AUG-1998; 98US-0097979P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099815P.
 PR 16-SEP-1998; 98US-0100827P.
 PR 16-SEP-1998; 98US-0100862P.
 PR 16-SEP-1998; 98US-0100863P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 22-SEP-1998; 98US-0100930P.
 PR 22-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021194.
 PR 22-DEC-1999; 99WO-US030720.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032378.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski EJ;
 Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2002-731348/79.
 P-PSDB; ABG95913.

New isolated secreted and transmembrane PRO polypeptide useful for
 modulating biological activity of a cell, or for treating sports-related
 joint problems, osteoarthritis or rheumatoid arthritis.

Claim 2; Fig 125; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO
 polypeptide having 80 % sequence identity to a sequence appearing as
 ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
 extracellular domain of the proteins with their associated signal peptide
 or lacking its associated signal peptide. Also included are the nucleic
 acids encoding the proteins, vectors, host cells, fusion proteins and

antibodies which specifically bind to the proteins. The proteins are useful for detecting a polypeptide designated as A, B, C or D in a sample suspected of containing an A, B, C or D polypeptide, by contacting the sample with a polypeptide designated as E, F, G, H or I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide conjugate in the sample, where the formation of the conjugate is indicative of the presence of an A, B, C or D polypeptide in the sample, where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO3801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with a detectable label or is attached to a solid support. The proteins are useful for linking a bioactive molecule to a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies against them are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I. The cell is killed. The proteins are useful for identifying agonists or antagonists, for the preparation of a medicament useful in the treatment of a condition which is responsive to the proteins, as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. Nucleic acids encoding the proteins are useful as hybridization probes, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, for the preparation of the proteins, to generate transgenic or knockout animals which are useful in the development and screening of therapeutic useful reagents, for chromosome identification, and in gene therapy. The antibody is useful as a therapeutic agent, in a diagnostic assay and for affinity purification of the protein from recombinant cell culture natural sources. The present sequence encodes a novel secreted or transmembrane protein of the invention.

Query Match 96.1%; Score 998; DB 6; Length 998;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

14 CGTTATCGTTCGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 73
1 CGTTATCGTTCGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 60
74 CGCTGACCCAGATGCGCCCGAGCGAGCAAAATCTCTGTCGCGCTGCGGCTACCG 133
61 CGCTGACCCAGATGCGCCCGAGCGAGCAAAATCTCTGTCGCGCTGCGGCTACCG 120
134 TGCCCGAGCTAGCAACCTTTCCCTCGATCTCAAAAACTCCAAATGCAAGGAG 193
121 TGCCCGAGCTAGCAACCTTTCCCTCGATCTCAAAAACTCCAAATGCAAGGAG 180
194 AAGCAGCTCTTGCTCGGTTGGGAGCGGTGCAAGAGAATCTGCCCTATAGGGGAATGG 253
181 AAGCAGCTCTTGCTCGGTTGGGAGCGGTGCAAGAGAATCTGCCCTATAGGGGAATGG 240
254 TGGGCAAGCCCTAGGATCATTTGAAGAGAGAGGCTTTCTAAAGCTTTGGCAAGAGTGA 313
241 TGGGCAAGCCCTAGGATCATTTGAAGAGAGAGGCTTTCTAAAGCTTTGGCAAGAGTGA 300
314 CACCCGCCATTTACAGACAGTGTATCTATCTGAGGTGCAATGTCACATATGACATC 373
301 CACCCGCCATTTACAGACAGTGTATCTATCTGAGGTGCAATGTCACATATGACATC 360
374 TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAGCATTTATCCCTTTTGGAAATCAGTCA 433
361 TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAGCATTTATCCCTTTTGGAAATCAGTCA 420
434 TTGGAGGATGATGCTGTGTTTATTTGGCCAGTTTTAGCCAAATCAAACTGACCTAGTGA 493
421 TTGGAGGATGATGCTGTGTTTATTTGGCCAGTTTTAGCCAAATCAAACTGACCTAGTGA 480

QY 494 AGGTTTCAGATGCAATGGAAGGAAAAAGAACTGGAGGAAACCACTTGGATTTCGTG 553
DB 481 AGGTTTCAGATGCAATGGAAGGAAAAAGAACTGGAGGAAACCACTTGGATTTCGTG 540
QY 554 GTCTACATCATGCAATTTGCAAAATCTTAGCTGAAGAGGAATACGAGGCTTTGGGCGAG 613
DB 541 GTCTACATCATGCAATTTGCAAAATCTTAGCTGAAGAGGAATACGAGGCTTTGGGCGAG 600
QY 614 GCTGGGTACCCCAATATACAAAGAGGAGCACTGGTGAATATGGGAGATTTAACCACTTATG 673
DB 601 GCTGGGTACCCCAATATACAAAGAGGAGCACTGGTGAATATGGGAGATTTAACCACTTATG 660
QY 674 ATACAGTGAACCACTACTTGGTATTGAATACACCACTTGAAGGACAATATCATGACTCAGC 733
DB 661 ATACAGTGAACCACTACTTGGTATTGAATACACCACTTGAAGGACAATATCATGACTCAGC 720
QY 734 GTTTATCAAGTTTATGTTCTGAGCTGGTACTTCTATTTCTGGAAACACGAGCGATGCA 793
DB 721 GTTTATCAAGTTTATGTTCTGAGCTGGTACTTCTATTTCTGGAAACACGAGCGATGCA 780
QY 794 TCAAAAGCAGAAATGAATCAACACGAGATAAACAGGAGGGGACTTTTGTATTAAT 853
DB 781 TCAAAAGCAGAAATGAATCAACACGAGATAAACAGGAGGGGACTTTTGTATTAAT 840
QY 854 CATCGACTCACTGCTTGTGATTCAAGGTCAAGGATTTCATGAGTCTATATAAAG 913
DB 841 CATCGACTCACTGCTTGTGATTCAAGGTCAAGGATTTCATGAGTCTATATAAAG 900
QY 914 GCTTTTACCATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 973
DB 901 GCTTTTACCATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 960
QY 974 AAAAAATCAGAGATGAGTGGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1011
DB 961 AAAAAATCAGAGATGAGTGGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 998

RESULT 6
ACA91226
ID ACA91226 standard; cDNA; 998 BP.
XX
ACA91226;
AC
AC
DT 11-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1566 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; antibody therapy;
KW pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.
OS Homo sapiens.
XX
US2003018173-A1.
PN
XX
PD 23-JAN-2003.
XX
PF 01-MAY-2002; 2002US-00063515.
XX
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-401702/38.
XX
DR P-PSDB; ABU90938.
XX
PT New antibody useful for identifying PRO polypeptides, for affinity
PT purification of PRO polypeptides, and for preparing a medicament
PT diagnosing or treating conditions responsive to the antibody or PRO
PT polypeptide.

PR	18-JUL-2001; 2001US-00908827.	Db	481	AGGTTTCAGATGCAATGGAAGGAAAAAGGAAACCTGGAAGAAACCAATTCGATTCGTG	540
XX	06-DEC-2001; 2001US-00006867.	QY	554	GTGTACATCATGCTTTGCAAAAATCTTAGCTGAAGAGGAATACAGAGGCTTTTGGGCGAG	613
PA	(GETH) GENENTECH INC.	Db	541	GTGTACATCATGCTTTGCAAAAATCTTAGCTGAAGAGGAATACAGAGGCTTTTGGGCGAG	600
XX	Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;	QY	614	GCTGGGTACCCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG	673
PI	Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;	Db	601	GCTGGGTACCCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG	660
XX	P-PSDB; ABO33997.	QY	674	ATACAGTGAACCACTACTTGGTATTGAATACACCACTTGGGAGCAATATCATGACTCACG	733
PT	New isolated antibody specifically binding a PRO polypeptide, useful for	Db	661	ATACAGTGAACCACTACTTGGTATTGAATACACCACTTGGGAGCAATATCATGACTCACG	720
PT	the preparation of a medicament for treating disorders with the aberrant	QY	734	GTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTTGGGAAACACAGCCGATGCA	793
PT	expression or activity of the PRO polypeptide, such as tumor conditions	Db	721	GTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTTGGGAAACACAGCCGATGCA	780
PS	and cancer.	QY	794	TCAAAAGCAGAATAATGAATCAACACGAGATATAACAGGAAGGGGACTTTTGTATAAAT	853
XX	Disclosure; Fig 125; 223pp; English.	Db	781	TCAAAAGCAGAATAATGAATCAACACGAGATATAACAGGAAGGGGACTTTTGTATAAAT	840
CC	The invention relates to an antibody that binds to a secreted or	QY	854	CATCGACTGACTGCTTTGATTTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAG	913
CC	transmembrane protein designated PRO1446 appearing as ABO33941. The	Db	841	CATCGACTGACTGCTTTGATTTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAG	900
CC	protein is one of 84 PRO polypeptides which (along with their encoding	QY	914	GCTTTTACCATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG	973
CC	nucleic acids) are disclosed in the specification. The methods and	Db	901	GCTTTTACCATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG	960
CC	compositions of the present invention are useful for the preparation of a	QY	974	AAAAATCAGAGAGATGAGTGGAGTCAAGTCCATTTTAA 1011	
CC	medicament for the treatment of disorders associated with the aberrant	Db	961	AAAAATCAGAGAGATGAGTGGAGTCAAGTCCATTTTAA 998	
CC	expression or activity of the PRO polypeptide, such as tumour conditions	XX	RESULT 8		
CC	and cancer. They can also be used to generate transgenic or knockout	XX	ACA60425		
CC	animals useful in the development and screening of therapeutically useful	ID	ACA60425 standard; cDNA; 998 BP.		
CC	reagents. The PRO polypeptides and encoding nucleic acids can be used as	AC	ACA60425;		
CC	molecular weight markers for protein electrophoresis, chromosome	XX	11-JUN-2003 (first entry)		
CC	identification and tissue typing. The antibodies may be used in various	DT	Novel human secreted and transmembrane protein PRO1566 cDNA.		
CC	diagnostic, competitive binding and/or immunoprecipitation assays. The	XX	Human; secreted and transmembrane polypeptide; gene;		
CC	present sequence encodes a PRO polypeptide	XX	ss. chromosome mapping; gene mapping; transgenic animal; knockout animal;		
XX	Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;	XX	therapeutic agent screening; chromosome identification; tissue typing;		
QY		OS	gene therapy.		
Best Match	96.1%; Score 998; DB 7; Length 998;	XX	Homo sapiens.		
Best Local Similarity	100.0%; Pred. No. 0;	XX	US2003018183-A1.		
Matches	998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	23-JAN-2003.		
QY	14 CCGTTATCGTTGCGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 73	XX	01-MAY-2002; 2002US-00063512.		
Db	1 CCGTTATCGTTGCGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 60	XX	06-DEC-2001; 2001US-00006867.		
QY	74 CGCTGACCCAGAGATGCCCGGAGCGAGCAAAATCTCTACTGTCCGGCTGCGCGGTACCG 133	XX	(GETH) GENENTECH INC.		
Db	61 CGCTGACCCAGAGATGCCCGGAGCGAGCAAAATCTCTACTGTCCGGCTGCGCGGTACCG 120	PI	Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;		
QY	134 TGGCCGAGCTAGCAACTTTCCCTCGATCTCAAAAACTCGACTCCCAATGCAAGGAG 193	PI	Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;		
Db	121 TGGCCGAGCTAGCAACTTTCCCTCGATCTCAAAAACTCGACTCCCAATGCAAGGAG 180	XX	WPI; 2003-330984/31.		
QY	194 AAGCAGCTCTTGTCTCGGTTGGGAGCGGTGCAAGAGAAATCTGCCCTATAGGGGAATGG 253	DR	P-PSDB; ABU72014.		
Db	181 AAGCAGCTCTTGTCTCGGTTGGGAGCGGTGCAAGAGAAATCTGCCCTATAGGGGAATGG 240	XX	New secreted and transmembrane PRO polypeptides and nucleic acid		
QY	254 TGGCCACAGCCCTAGGATCATTTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAGGAGTGA 313	PT	molecules encoding the polypeptides, useful in gene therapy or preparing		
Db	241 TGGCCACAGCCCTAGGATCATTTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAGGAGTGA 300	PT	a medicament for treating a condition that is responsive to the PRO		
QY	314 CACCCGCGCAATTTACAGACAGTATGATTTCTGGAGTGAATGGTCAATATGAACATC 373	XX	polypeptide or antibody.		
Db	301 CACCCGCGCAATTTACAGACAGTATGATTTCTGGAGTGAATGGTCAATATGAACATC 360	XX			
QY	374 TCCGAGAGTTGTTTGGCAAAAGTGAAGATGAGCAATATCCCTTTGGAATCATGTC 433	XX			
Db	361 TCCGAGAGTTGTTTGGCAAAAGTGAAGATGAGCAATATCCCTTTGGAATCATGTC 420	XX			
QY	434 TTGGAGGAGTATGAGTGGTGGTGTATTGGCCAGTGTATTAGCCAAATCAACTGACTAGTGA 493	XX			
Db	421 TTGGAGGAGTATGAGTGGTGGTGTATTGGCCAGTGTATTAGCCAAATCAACTGACTAGTGA 480	XX			
QY	494 AGGTTTCAGATGCAAAATGGAAGGAAAAAGGAAACCTGGAAGGAAACCAATTCGATTCGTG 553	XX			

PS Disclosure; Fig 125; 409pp; English.

XX The invention describes novel isolated PRO polypeptides. The PRO
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA and
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This sequence encodes a novel human secreted
CC and transmembrane PRO polypeptide

SQ Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;

Query Match 96.1%; Score 998; DB 7; Length 998;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	14	CCGTTATCGTCTTGGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC	73
Db	1	CCGTTATCGTCTTGGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC	60
QY	74	CGCTGACCCAGAGATGCGCCGAGCGAGCAAAATCTCTACTGTCCGGCTGCGGCTACCG	133
Db	61	CGCTGACCCAGAGATGCGCCGAGCGAGCAAAATCTCTACTGTCCGGCTGCGGCTACCG	120
QY	134	TGGCGGAGCTAGCAACTTCCCTCGGATCTCAGAAAATCTCGATCTCAAAATGCAAGGAG	193
Db	121	TGGCGGAGCTAGCAACTTCCCTCGGATCTCAGAAAATCTCGATCTCAAAATGCAAGGAG	180
QY	194	AAGCAGCTCTTGTCTCGTGTGGAGACGCTGCAAGAGAAATCTGCCCTATAGGGGAATGG	253
Db	181	AAGCAGCTCTTGTCTCGTGTGGAGACGCTGCAAGAGAAATCTGCCCTATAGGGGAATGG	240
QY	254	TGCCACAGCCCTAGGATCATTTGAAGAGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA	313
Db	241	TGCCACAGCCCTAGGATCATTTGAAGAGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA	300
QY	314	CACCCGCAATTACAGACAGTGTATCTGAGGTGCAATGGTCAATATGAACATC	373
Db	301	CACCCGCAATTACAGACAGTGTATCTGAGGTGCAATGGTCAATATGAACATC	360
QY	374	TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAGCAATATCCCTTTTGAAATCAGTCA	433
Db	361	TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAGCAATATCCCTTTTGAAATCAGTCA	420
QY	434	TTGGAGGATGATGGCTGTGTTATTTGGCCAGTCTTTAGCCATTCGAATGAGCTAGTGA	493
Db	421	TTGGAGGATGATGGCTGTGTTATTTGGCCAGTCTTTAGCCATTCGAATGAGCTAGTGA	480
QY	494	AGGTTTCAGATGCAATGGAAGGAAAGGAAATCTGGAAGGAAACCATTCGAGTTTCGTCG	553
Db	481	AGGTTTCAGATGCAATGGAAGGAAAGGAAATCTGGAAGGAAACCATTCGAGTTTCGTCG	540
QY	554	GTGTATCATGCAATTTGCAAAATCTTAGCTGAAGAGGAAATACGAGGCTTTGGGCGAG	613
Db	541	GTGTATCATGCAATTTGCAAAATCTTAGCTGAAGAGGAAATACGAGGCTTTGGGCGAG	600
QY	614	GCTGGGTACCAATATACGAAGAGCAGCTGCTGTAATGAGGATTTAAACCACTATG	673
Db	601	GCTGGGTACCAATATACGAAGAGCAGCTGCTGTAATGAGGATTTAAACCACTATG	660
QY	674	ATACAGTGAACACTACTTGGTATTGAATACACCACTTTGAGGACAATATCATGACTCAGG	733
Db	661	ATACAGTGAACACTACTTGGTATTGAATACACCACTTTGAGGACAATATCATGACTCAGG	720

QY	734	GTTTATCAAGTTTATGTTCTGGACTGCTAGCTTCTATTCTGGGAACACACGAGCCGATGTC	793
Db	721	GTTTATCAAGTTTATGTTCTGGACTGCTAGCTTCTATTCTGGGAACACACGAGCCGATGTC	780
QY	794	TCAAAAGCAGAAATTAATGAATCAACACGAGATATAACAAAGGAGGAGCTTTTGTATAAAT	853
Db	781	TCAAAAGCAGAAATTAATGAATCAACACGAGATATAACAAAGGAGGAGCTTTTGTATAAAT	840
QY	854	CATCGACTGACTGCTTGAATTCAGGCTGTTTCAAGGTGAAGGATTCATGAGTCTATATAAAG	913
Db	841	CATCGACTGACTGCTTGAATTCAGGCTGTTTCAAGGTGAAGGATTCATGAGTCTATATAAAG	900
QY	914	GCTTTTACCACCTTGGCTGAGATCAACCCCTTGGTCAATGGTGTCTGGCTTACTTATG	973
Db	901	GCTTTTACCACCTTGGCTGAGATCAACCCCTTGGTCAATGGTGTCTGGCTTACTTATG	960
QY	974	AAAAAATCAGAGAGATGAGTGGAGTCAAGTCCATTTTAA	1011
Db	961	AAAAAATCAGAGAGATGAGTGGAGTCAAGTCCATTTTAA	998
RESULT 9			
ACA58872			
ID	ACA58872 standard; cDNA; 998 BP.		
XX	ACA58872;		
AC	ACA58872;		
XX	ACA58872;		
DT	10-JUN-2003 (first entry)		
XX	cDNA encoding human secreted polypeptide PRO1566.		
DE	Human; ss; gene; gene therapy; tumour; cancer.		
KW	Human; ss; gene; gene therapy; tumour; cancer.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	US2003013855-A1.		
PN	16-JAN-2003.		
XX	03-MAY-2002; 2002US-00063616.		
PF	30-DEC-1998; 98KR-00062142.		
XX	08-MAR-1999; 99WO-US0005028.		
PR	14-MAY-1999; 99US-00311832.		
PR	14-MAY-1999; 99WO-US010733.		
PR	25-AUG-1999; 99US-00380137.		
PR	25-AUG-1999; 99US-00380138.		
PR	25-AUG-1999; 99US-00380139.		
PR	25-AUG-1999; 99US-00380142.		
PR	15-SEP-1999; 99US-00397342.		
PR	18-OCT-1999; 99US-00403297.		
PR	12-NOV-1999; 99US-00423844.		
PR	30-DEC-1999; 99WO-US01274.		
PR	18-FEB-2000; 2000WO-US004341.		
PR	01-MAR-2000; 2000WO-US005601.		
PR	02-MAR-2000; 2000WO-US005841.		
PR	21-MAR-2000; 2000WO-US007532.		
PR	22-JUN-2000; 2000WO-US014042.		
PR	22-AUG-2000; 2000US-00644848.		
PR	24-AUG-2000; 2000WO-US023328.		
PR	18-SEP-2000; 2000US-00664610.		
PR	18-SEP-2000; 2000US-00665350.		
PR	08-NOV-2000; 2000US-00709238.		
PR	10-NOV-2000; 2000WO-US030873.		
PR	01-DEC-2000; 2000WO-US032678.		
PR	20-DEC-2000; 2000US-00747259.		
PR	20-DEC-2000; 2000WO-US034956.		
PR	28-FEB-2001; 2001WO-US006520.		
PR	22-MAR-2001; 2001US-00816744.		
PR	10-MAY-2001; 2001US-00854208.		
PR	10-MAY-2001; 2001US-00854280.		
PR	30-MAY-2001; 2001US-00870574.		

PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 29-JUN-2001; 2001US-00869599.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-DEC-2001; 2001US-00006867.
 XX (GETH) GENENTECH INC.
 PA
 XX
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX
 XX WPI; 2003-330485/31.
 DR P-PSDB; ABU71568.
 XX
 XX New isolated antibody specifically binding a PRO polypeptide, useful for
 PT the preparation of a medicament for treating disorders with the aberrant
 PT expression or activity of the PRO polypeptide, such as tumor conditions
 PT and cancer.
 XX
 PS Example 4; Page 198; 406pp; English.
 CC
 CC The invention relates to an antibody that binds to a polypeptide with a
 CC fully defined sequence given in the specification. The methods and
 CC compositions (containing antibodies that specifically bind a PRO
 CC polypeptide) of the present invention are useful for the preparation of a
 CC medicament for the treatment of disorders associated with the aberrant
 CC expression or activity of the PRO polypeptide, such as tumour conditions
 CC and cancer. They can also be used to generate transgenic or knockout
 CC animals useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
 CC molecular weight markers for protein electrophoresis, chromosome
 CC identification and tissue typing. The PRO polypeptides are useful to
 CC induce angiogenesis e.g wound healing; in the treatment of sports-related
 CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid
 CC arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The
 CC antibodies may be used in various diagnostic, competitive binding and/or
 CC immunoprecipitation assays. The present sequence represents a cDNA
 CC encoding a PRO polypeptide of the invention
 XX
 SQ Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;

Query Match 96.1%; Score 998; DB 7; Length 998;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CGCTTATCGTTCGCGTACTGCTGAATGTCCTCCGCGGAGGAGGAGGCGCTTTTCG 73
 DB 1 CGCTTATCGTTCGCGTACTGCTGAATGTCCTCCGCGGAGGAGGAGGCGCTTTTCG 60
 QY 74 CGCTGACCCAGAGATGCGCCCGGAGCGAGCAAAATTCCTACTGTCGCGGCTACCG 133
 DB 61 CGCTGACCCAGAGATGCGCCCGGAGCGAGCAAAATTCCTACTGTCGCGGCTACCG 120
 QY 134 TGGCCGAGCTAGCAACCTTTCCCTCGATCTCAAAAACTCGACTTCCAAATGCAAGGAG 193
 DB 121 TGGCCGAGCTAGCAACCTTTCCCTCGATCTCAAAAACTCGACTTCCAAATGCAAGGAG 180
 QY 194 AAGCAGCTCTTGCTCGGTTGGGAGCGGTGCAAGAGAAATCGCCCTATAGGGGAATCG 253
 DB 181 AAGCAGCTCTTGCTCGGTTGGGAGCGGTGCAAGAGAAATCGCCCTATAGGGGAATCG 240
 QY 254 TGGCCAGCCCTTAGGAGTCAATGAAGAGGAAGGCTTTCTAAAGCTTTTGGCAAGAGTGA 313
 DB 241 TGGCCAGCCCTTAGGAGTCAATGAAGAGGAAGGCTTTCTAAAGCTTTTGGCAAGAGTGA 300
 QY 314 CACCCGCCAATTTACAGACAGTGTGTATTTCTGGAGGTGCAATGGTCAATATGAACATC 373
 DB 301 CACCCGCCAATTTACAGACAGTGTGTATTTCTGGAGGTGCAATGGTCAATATGAACATC 360
 QY 374 TCCGAGAGGTTGTTTGGCAAAAGTGAAGATGAGCATTTATCCCTTTTGGAAATCAGTCA 433
 DB 361 TCCGAGAGGTTGTTTGGCAAAAGTGAAGATGAGCATTTATCCCTTTTGGAAATCAGTCA 420

QY 434 TTGGAGGGATGATGGCTGCTGTTTATTTGGCCAGTCTTTTAGCCAAATCCAACCTAGCTAGTGA 493
 DB 421 TTGGAGGGATGATGGCTGCTGTTTATTTGGCCAGTCTTTTAGCCAAATCCAACCTAGTGA 480
 QY 494 AGGTTTCAGATGCAGATGGAAGGAAAAAGGAACTGGAAGGAAAAACCATTTGCGATTTTCGTG 553
 DB 481 AGGTTTCAGATGCAGATGGAAGGAAAAAGGAACTGGAAGGAAAAACCATTTGCGATTTTCGTG 540
 QY 554 GTGTACATCATGCTATTTGCAAAATCTTAGCTGAAGGAGGAATACAGAGGCTTTTGGGCAG 613
 DB 541 GTGTACATCATGCTATTTGCAAAATCTTAGCTGAAGGAGGAATACAGAGGCTTTTGGGCAG 600
 QY 614 GCTGGGTACCCAAATATACAAAGAGCAGCACTGGTGAATATGGAGATTTTAAACCACTTATG 673
 DB 601 GCTGGGTACCCAAATATACAAAGAGCAGCACTGGTGAATATGGAGATTTTAAACCACTTATG 660
 QY 674 ATACAGTGAACACTTACTTTGGTATTTGAATACACCCTTGAGGACAATATCATGACTCAGC 733
 DB 661 ATACAGTGAACACTTACTTTGGTATTTGAATACACCCTTGAGGACAATATCATGACTCAGC 720
 QY 734 GTTTATCAAGTTTATGTTCTGCACTGCTAGCTTCTATTCTGGGAACACACAGCCGATGTCA 793
 DB 721 GTTTATCAAGTTTATGTTCTGCACTGCTAGCTTCTATTCTGGGAACACACAGCCGATGTCA 780
 QY 794 TCAAAAGCAGATAAATAATCAACACAGAGATAAACAAGAGGGGACTTTTGTATAAAT 853
 DB 781 TCAAAAGCAGATAAATAATCAACACAGAGATAAACAAGAGGGGACTTTTGTATAAAT 840
 QY 854 CATCGACTGACTGCTTGTATTCAGGCTGTTCAAGGTGAAGGATTCATGACTATATAAAG 913
 DB 841 CATCGACTGACTGCTTGTATTCAGGCTGTTCAAGGTGAAGGATTCATGACTATATAAAG 900
 QY 914 GCTTTTTCACATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATG 973
 DB 901 GCTTTTTCACATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATG 960
 QY 974 AAAAAATCAGAGATGAGTGGAGTCAGTCCCAATTTTAA 1011
 DB 961 AAAAAATCAGAGATGAGTGGAGTCAGTCCCAATTTTAA 998
 RESULT 10
 ID ACA64048 standard; cDNA; 998 BP.
 XX ACA64048;
 AC ACA64048;
 XX
 DT 16-JUN-2003 (first entry)
 XX
 DE cDNA encoding human PRO polypeptide #63.
 XX
 KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW anti-PRO antibody; diagnostic assay; gene expression; gene; ss.
 XX Homo sapiens.
 OS
 PN US2002182638-A1.
 XX
 PD 05-DEC-2002.
 XX
 PF 02-MAY-2002; 2002US-00063547.
 XX
 PR 30-DEC-1998; 98KR-00062142.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99US-0031832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380142.
 PR 15-SEP-1999; 99US-00397342.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.

PR	30-DEC-1999;	99WO-US031274.	
PR	18-FEB-2000;	2000WO-US04341.	
PR	01-MAR-2000;	2000WO-US005601.	
PR	02-MAR-2000;	2000WO-US005841.	
PR	21-MAR-2000;	2000WO-US007532.	
PR	22-MAR-2000;	2000WO-US014042.	
PR	02-JUN-2000;	2000WO-US015264.	
PR	22-AUG-2000;	2000US-00644848.	
PR	24-AUG-2000;	2000WO-US023328.	
PR	18-SEP-2000;	2000US-00664610.	
PR	18-SEP-2000;	2000US-00665350.	
PR	08-NOV-2000;	2000US-00709238.	
PR	10-NOV-2000;	2000WO-US030873.	
PR	01-DEC-2000;	2000WO-US032878.	
PR	20-DEC-2000;	2000US-00747259.	
PR	20-DEC-2000;	2000WO-US034956.	
PR	28-FEB-2001;	2001WO-US006520.	
PR	22-MAR-2001;	2001US-00816744.	
PR	10-MAY-2001;	2001US-00854208.	
PR	30-MAY-2001;	2001US-00870574.	
PR	01-JUN-2001;	2001WO-US017800.	
PR	05-JUN-2001;	2001US-00874503.	
PR	29-JUN-2001;	2001US-00869599.	
PR	18-JUL-2001;	2001US-00908827.	
PR	06-DEC-2001;	2001US-00006867.	
XX			
PA	(GETH)	GENENTECH INC.	
XX			
PI	Eaton DL, Filvaroff E, Gertitsen ME, Goddard A, Godowski PJ;		
PI	Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;		
XX			
DR	WPI; 2003-328612/04.		
XX	P-PSDB; ABU72349.		
PT	An isolated secreted transmembrane polypeptide designated PRO, useful as		
PT	a therapeutic agent.		
XX			
PS	Disclosure; Fig 125; 236pp; English.		
XX			
CC	The present invention relates to the isolation of novel human PRO		
CC	polypeptides, and the polynucleotide sequences encoding them. The PRO		
CC	polypeptides are secreted and transmembrane proteins. The PRO		
CC	polypeptides and polynucleotides are useful for preparing a medicament		
CC	useful in the treatment of a condition responsive to anti-PRO antibody.		
CC	Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting		
CC	its expression in specific cells, tissues or serum, and for affinity		
CC	purification of PRO from recombinant cell culture or natural sources.		
CC	ACA63986-ACA64069 represent cDNA sequences encoding the human PRO		
CC	polypeptides of the invention		
XX			
SQ	Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;		
Query Match	96.1%; Score 998; DB 7; Length 998;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 998;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	14	CCGTTATCGTCTTCGGCTACTGCTGAATGTCGTCGCGAGGAGGAGGAGGCTTTTGC	73
DB	1	CCGTTATCGTCTTCGGCTACTGCTGAATGTCGTCGCGAGGAGGAGGAGGCTTTTGC	60
QY	74	CGCTGACCCAGAGATGCGCGAGCGAGCAAAATTCCTACTGTCGCGTCCGCGCTACCG	133
DB	61	CGCTGACCCAGAGATGCGCGAGCGAGCAAAATTCCTACTGTCGCGTCCGCGCTACCG	120
QY	134	TGCGCGAGCTAGCAACCTTTCCCTGGATCTCAAAAATCGACTCCAAATGCAAGGAG	193
DB	121	TGCGCGAGCTAGCAACCTTTCCCTGGATCTCAAAAATCGACTCCAAATGCAAGGAG	180
QY	194	AAGCAGCTCTTGTCTGGTCTGGGAGCGGTCAGAGAAATCTGCCCTATAGGGGAATGG	253
DB	181	AAGCAGCTCTTGTCTGGTCTGGGAGCGGTCAGAGAAATCTGCCCTATAGGGGAATGG	240

QY	254	TGCGCACAGCCCTAGGGATCAATGAAGAGGAGGCTTCTAAAGCTTTGGCAAGGAGTGA	313
DB	241	TGCGCACAGCCCTAGGGATCAATGAAGAGGAGGCTTCTAAAGCTTTGGCAAGGAGTGA	300
QY	314	CACCCGCCATTTACAGACACGTAAGTGTATTCGAGAGTGAATGGTCAATATGAACATC	373
DB	301	CACCCGCCATTTACAGACACGTAAGTGTATTCGAGAGTGAATGGTCAATATGAACATC	360
QY	374	TCCGAGAGGTTGTGTTTGGCAAAAGTGAAGATGAGCATTAATCCCTTTGGAATCAAGTCA	433
DB	361	TCCGAGAGGTTGTGTTTGGCAAAAGTGAAGATGAGCATTAATCCCTTTGGAATCAAGTCA	420
QY	434	TTGGAGGGATGATGGCTGGTGTATTTGGCCAGTTTATAGCCANTCAACTGACTAGTGA	493
DB	421	TTGGAGGGATGATGGCTGGTGTATTTGGCCAGTTTATAGCCANTCAACTGACTAGTGA	480
QY	494	AGGTTTCAGATGCAAAATGGAAGGAAAGAAATCGAAGGAAACCAATTCGGAATTCGTG	553
DB	481	AGGTTTCAGATGCAAAATGGAAGGAAAGAAATCGAAGGAAACCAATTCGGAATTCGTG	540
QY	554	GTGTATCATGCAATTTGCAAAATCTTAGCTGAAGAGGAATACGAGGGCTTTGGGCAG	613
DB	541	GTGTATCATGCAATTTGCAAAATCTTAGCTGAAGAGGAATACGAGGGCTTTGGGCAG	600
QY	614	GCTGGGTACCCATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTATG	673
DB	601	GCTGGGTACCCATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTATG	660
QY	674	ATACAGTGAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCACG	733
DB	661	ATACAGTGAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCACG	720
QY	734	GTTTATCAAGTTTATGTTCTGGACTGGTACTTCTATTTCTGGGAAACACAGCCGATGTC	793
DB	721	GTTTATCAAGTTTATGTTCTGGACTGGTACTTCTATTTCTGGGAAACACAGCCGATGTC	780
QY	794	TCAAAAGCAGATAATGAATCAACACGAGATAAACAAGAGGGGACTTTTGTATATAAT	853
DB	781	TCAAAAGCAGATAATGAATCAACACGAGATAAACAAGAGGGGACTTTTGTATATAAT	840
QY	854	CATCGACTGACTGCTTGTGATTTCAGGCTGTTCAAGGTGAAGGATTCATGACTATATAAG	913
DB	841	CATCGACTGACTGCTTGTGATTTCAGGCTGTTCAAGGTGAAGGATTCATGACTATATAAG	900
QY	914	GCTTTTACCACTTGGCTGAGATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATG	973
DB	901	GCTTTTACCACTTGGCTGAGATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATG	960
QY	974	AAAAATCAGAGAGATGAGTGGAGTCAGTCCATTTTAA	1011
DB	961	AAAAATCAGAGAGATGAGTGGAGTCAGTCCATTTTAA	998

RESULT 11
 ACA91312
 ID ACA91312 standard; cDNA; 998 BP.
 XX ACA91312;
 AC ACA91312;
 XX
 DT 14-JUL-2003 (first entry)
 XX
 DE cDNA encoding human PRO polypeptide #63.
 XX
 KW Human; PRO polypeptide; secreted protein; transmembrane protein; rectal;
 KW lung; stomach; oesophageal; skin; tumour; cancer; cytosolic;
 KW gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003018168-A1.
 XX
 PD 23-JAN-2003.
 XX

PF 02-MAY-2002; 2002US-00063569.
 XX 30-DEC-1998; 98KR-00062142.
 PR 08-MAR-1999; 99WO-US0005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380142.
 PR 15-SEP-1999; 99US-00397342.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 30-DEC-1999; 99WO-US031274.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 28-FEB-2001; 2000WO-US034956.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 29-JUN-2001; 2001US-00869599.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-DEC-2001; 2001US-00006867.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX
 XX WPI; 2003-401699/38.
 DR P-PSDB; ABU91022.
 DR
 XX
 XX New isolated, secreted and transmembrane PRO polypeptide, useful for the
 PT diagnosis, prevention and treatment of rectal, lung, stomach, esophageal
 PT or skin cancers.
 PT
 XX
 PS Disclosure; Fig 125; 235pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO polypeptide
 CC and polynucleotide sequences are useful for the diagnosis, prevention and
 CC treatment of rectal, lung, stomach, oesophageal or skin tumours, and/or
 CC cancers. The PRO polypeptides are also useful as molecular weight
 CC markers. The PRO polynucleotide sequences are useful for chromosome
 CC identification, hybridisation probes, and for screening libraries of
 CC human cDNA, genomic DNA or mRNA. They may also be used in gene therapy,
 CC particularly for replacing a defective gene. ACA91250-ACA91333 represent
 CC cDNA sequences encoding the human PRO polypeptides of the invention
 XX
 SQ Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;

Query Match 96.1%; Score 998; DB 7; Length 998;
 Best Local Similarity 100.0%; Pred. NO. 0;
 Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 14 CCCTTATCGTCTTGGCGCTACTGCTGAATGTCCGCGAGGAGGAGGAGGCTTTTGC 73

1	CCGTTATCGTCTTGGCGCTACTGCTGAATGTCCGCGAGGAGGAGGCTTTTGC	60
74	CGCTGACCCAGAGATGCCCGGAGGAGCAAAATCTCTACTGTCCGGCTGCGCGCTACCG	133
61	CGCTGACCCAGAGATGCCCGGAGGAGCAAAATCTCTACTGTCCGGCTGCGCGCTACCG	120
134	TGGCCGAGCTAGCAACCTTTCCCTCGATCTCAAAAAAATCGACCTCAAAATCAAGGAG	193
121	TGGCCGAGCTAGCAACCTTTCCCTCGATCTCAAAAAAATCGACCTCAAAATCAAGGAG	180
194	AAGCAGCTCTTGTCTCGGTTGGGAGACGGTGAAGAGAAATCTGCCCTCTATAGGGGAATGG	253
181	AAGCAGCTCTTGTCTCGGTTGGGAGACGGTGAAGAGAAATCTGCCCTCTATAGGGGAATGG	240
254	TGGCAGACGCCCTAGGAGATCAATGAAGAGAGAGCTTTCTAAAGCTTTGGCAAGGAGTGA	313
241	TGGCAGACGCCCTAGGAGATCAATGAAGAGAGAGCTTTCTAAAGCTTTGGCAAGGAGTGA	300
314	CACCCGCCATTTACAGACACGTAAGTCTATCTCGAGGTGGAATGGTCAATATGAACATC	373
301	CACCCGCCATTTACAGACACGTAAGTCTATCTCGAGGTGGAATGGTCAATATGAACATC	360
374	TCCGAGAGGTTGTGTTGGCAAAAGTGAAGATGAGCATTAATCCCTTTGGAAATCAGTCA	433
361	TCCGAGAGGTTGTGTTGGCAAAAGTGAAGATGAGCATTAATCCCTTTGGAAATCAGTCA	420
434	TTGGAGGAGTGTGCTGGTGGTGTATTTGGCCAGTTTATAGCCCAATCAACCTGACTAGTGA	493
421	TTGGAGGAGTGTGCTGGTGGTGTATTTGGCCAGTTTATAGCCCAATCAACCTGACTAGTGA	480
494	AGGTTCCAGATGCAAAATGGAAGGAAAAAGAAATCGAAGGAAAAACCAATCCGATTTTCGTG	553
481	AGGTTCCAGATGCAAAATGGAAGGAAAAAGAAATCGAAGGAAAAACCAATCCGATTTTCGTG	540
554	GTGTACATCATGCTTTGGCAAAATCTTAGCTGAAGAGGAAATACAGAGGCTTTGGGCGAG	613
541	GTGTACATCATGCTTTGGCAAAATCTTAGCTGAAGAGGAAATACAGAGGCTTTGGGCGAG	600
614	GCTGGGTACCCATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAACCACTTATG	673
601	GCTGGGTACCCATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAACCACTTATG	660
674	ATACAGTGAACACACTCTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCACG	733
661	ATACAGTGAACACACTCTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCACG	720
734	GTTTATCAAGTTTATGTTCTGGACTGGTACTTCTATTTCTGGGAAACACCGCCGATGCA	793
721	GTTTATCAAGTTTATGTTCTGGACTGGTACTTCTATTTCTGGGAAACACCGCCGATGCA	780
794	TCAAAAGCAGATTAATGAATCAACAGGAGATTAACAGGAGGAGCTTTTCTATTAAT	853
781	TCAAAAGCAGATTAATGAATCAACAGGAGATTAACAGGAGGAGCTTTTCTATTAAT	840
854	CATCGACTGACTGCTTGAATTCAGGCTGTTCAAGGTCAAGGATTCATGAGTCTATATAAG	913
841	CATCGACTGACTGCTTGAATTCAGGCTGTTCAAGGTCAAGGATTCATGAGTCTATATAAG	900
914	GCTTTTACCATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG	973
901	GCTTTTACCATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG	960
974	AAAAATCAGAGATGAGTGGAGTCAAGTCCATTTTAA 1011	
961	AAAAATCAGAGATGAGTGGAGTCAAGTCCATTTTAA 998	

RESULT 12
 ACD45211
 ID ACD45211 standard; cDNA; 998 BP.
 XX
 AC ACD45211;

XX 11-SEP-2003 (first entry)

XX Human secreted/transmembrane polypeptide PRO1566 cDNA.

XX Human; ss; tumour; cancer; gene therapy; tissue typing; gene.

XX Homo sapiens.

XX US2003009012-A1.

XX 09-JAN-2003.

XX 01-MAY-2002; 2002US-00063517.

XX 30-DEC-1998; 98KR-00062142.

XX 08-MAR-1999; 99WO-US005028.

XX 14-MAY-1999; 99US-00311832.

XX 14-MAY-1999; 99WO-US010733.

XX 25-AUG-1999; 99US-00380137.

XX 25-AUG-1999; 99US-00380138.

XX 25-AUG-1999; 99US-00380139.

XX 25-AUG-1999; 99US-00380142.

XX 15-SEP-1999; 99US-00397342.

XX 18-OCT-1999; 99US-00403297.

XX 12-NOV-1999; 99US-00423844.

XX 30-DEC-1999; 99WO-US031274.

XX 18-FEB-2000; 2000WO-US004341.

XX 01-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005841.

XX 21-MAR-2000; 2000WO-US007532.

XX 22-MAY-2000; 2000WO-US014042.

XX 02-JUN-2000; 2000WO-US015264.

XX 22-AUG-2000; 2000US-00544848.

XX 24-AUG-2000; 2000WO-US023328.

XX 18-SEP-2000; 2000US-00664610.

XX 18-SEP-2000; 2000US-00665350.

XX 08-NOV-2000; 2000US-00709238.

XX 10-NOV-2000; 2000WO-US030873.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 28-FEB-2001; 2001WO-US034956.

XX 28-FEB-2001; 2001US-00816744.

XX 10-MAY-2001; 2001US-00854208.

XX 10-MAY-2001; 2001US-00854280.

XX 30-MAY-2001; 2001US-00870574.

XX 01-JUN-2001; 2001WO-US017800.

XX 05-JUN-2001; 2001US-00874503.

XX 29-JUN-2001; 2001US-00869599.

XX 18-JUL-2001; 2001US-00908827.

XX 06-DEC-2001; 2001US-00006867.

XX (SETH) GENENTECH INC.

XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2003-447383/42.
XX P-PSDB; ABO27343.

XX New isolated antibody specifically binding a PRO polypeptide, useful for
XX the preparation of a medicament for treating disorders with the aberrant
XX expression or activity of the PRO polypeptide, such as tumor conditions
XX and cancer.

XX Disclosure; Fig 125; 223pp; English.

XX The invention relates to an antibody that binds to a secreted and
XX transmembrane PRO polypeptide. The methods and compositions of the
XX present invention are useful for the preparation of a medicament for the
XX treatment of disorders associated with the aberrant expression or
XX activity of the PRO polypeptide, such as tumour conditions and cancer.

CC They can also be used to generate transgenic or knockout animals useful
CC in the development and screening of therapeutically useful reagents. The
CC PRO polypeptides and encoding nucleic acids can be used as molecular
CC weight markers for protein electrophoresis, chromosome identification and
CC tissue typing. The antibodies may be used in various diagnostic,
CC competitive binding and/or immunoprecipitation assays. The present
CC sequence represents a secreted and transmembrane PRO polypeptide cDNA

XX SQ Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;

Query Match 96.1%; Score 998; DB 7; Length 998;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCGTTATCGTCTTGGCGCTACTGCTGAATGTCCTCCCGAGGAGGAGGAGGCTTTTGC 73
DB 1 CCGTTATCGTCTTGGCGCTACTGCTGAATGTCCTCCCGAGGAGGAGGAGGCTTTTGC 60

QY 74 CGCTGACCCAGAGATGCGCCCGAGCGAGCAAAATTCCTACTGTCGGCTGCGCGCTACCG 133
DB 61 CGCTGACCCAGAGATGCGCCCGAGCGAGCAAAATTCCTACTGTCGGCTGCGCGCTACCG 120

QY 134 TGGCCGAGCTAGCAACCTTTCCCTCGATCTCAAAAACTCGACTCCAAATCAAGGAG 193
DB 121 TGGCCGAGCTAGCAACCTTTCCCTCGATCTCAAAAACTCGACTCCAAATCAAGGAG 180

QY 194 AGCAGCTCTTGTCTCGTTGGGAGCGGTGCAAGAGAAATCGCCCTATAGGGGAATGG 253
DB 181 AGCAGCTCTTGTCTCGTTGGGAGCGGTGCAAGAGAAATCGCCCTATAGGGGAATGG 240

QY 254 TGGCCAGCGCTTGGGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTTGGCAAGGAGTGA 313
DB 241 TGGCCAGCGCTTGGGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTTGGCAAGGAGTGA 300

QY 314 CACCCGCCATTTACAGACAGCTAGTGTATTTGGAGGTGCAATGGTCAATATGAACATC 373
DB 301 CACCCGCCATTTACAGACAGCTAGTGTATTTGGAGGTGCAATGGTCAATATGAACATC 360

QY 374 TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAGCAATATCCCTTTGGAAATCAGTCA 433
DB 361 TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAGCAATATCCCTTTGGAAATCAGTCA 420

QY 434 TTGGAGGGATGATGGTGGTGTATTATGGCCAGTTTTAGCCAAATCAATCTGACCTAGTGA 493
DB 421 TTGGAGGGATGATGGTGGTGTATTATGGCCAGTTTTAGCCAAATCAATCTGACCTAGTGA 480

QY 494 AGTTTCAGATGCAATGGAAGGAAAGAAACTGGAAGGAAACCAATTCGCAATTCGTG 553
DB 481 AGTTTCAGATGCAATGGAAGGAAAGAAACTGGAAGGAAACCAATTCGCAATTCGTG 540

QY 554 GTGTACATCATGCTTTGCAAAATCTTAGCTGAGGAGGAATACAGGGCTTTGGGCAG 613
DB 541 GTGTACATCATGCTTTGCAAAATCTTAGCTGAGGAGGAATACAGGGCTTTGGGCAG 600

QY 614 GCTGGGTACCCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 673
DB 601 GCTGGGTACCCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 660

QY 674 ATACAGTGAACACACTACTTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCAG 733
DB 661 ATACAGTGAACACACTACTTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCAG 720

QY 734 GTTTTCAAGTTTATGTTCTCGACTGGTGTCTTATTTCTGGGAAACACAGCGGATGTCA 793
DB 721 GTTTTCAAGTTTATGTTCTCGACTGGTGTCTTATTTCTGGGAAACACAGCGGATGTCA 780

QY 794 TCAAAAGCAGAATAATGAATCAACCAAGAGATAAACAAGAAAGGGAGCTTTTGTATAAT 853
DB 781 TCAAAAGCAGAATAATGAATCAACCAAGAGATAAACAAGAAAGGGAGCTTTTGTATAAT 840

QY 854 CATCGACTGACCTGCTGATTTCAGGCTGTTCAAGGTGAAGGATTCATGACTCTATATAAG 913
DB 841 CATCGACTGACCTGCTGATTTCAGGCTGTTCAAGGTGAAGGATTCATGACTCTATATAAG 900

		GCTTTTACCATCTTGGCTGAGATGAGCCCTTGTC	973
Qy	914	GCTTTTACCATCTTGGCTGAGATGAGCCCTTGTC	973
		CAATGGTGTCTTGCCTTACTTATG	
Db	901	GCTTTTACCATCTTGGCTGAGATGAGCCCTTGTC	960
		CAATGGTGTCTTGCCTTACTTATG	
Qy	974	AAAAAATCAGAGAGATGAGTGAGTCAGTCCATTAA	1011
Db	961	AAAAAATCAGAGAGATGAGTGAGTCAGTCCATTAA	998

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2003-392892/37.
P-PSDB: ABU92538.

New PRO994 polypeptide, useful for detecting tumors, or for stimulating Tumor Necrosis Factor alpha, or pericyte proliferation, especially for treating cancer, cartilage defects, osteoarthritis and rheumatoid arthritis in a mammal.

Disclosure; Fig 125; 235pp; English.

The invention relates to a new isolated PRO994 polypeptide, comprises an amino acid sequence appearing as ABUS24499, PRO994 lacking its associated signal peptide, the extracellular domain of, PRO994, the extracellular domain of PRO994 (lacking its associated signal peptide) or the protein encoded by the full-length coding sequence of the cDNA ATCC 203018. Also included is a chimeric molecule comprising the PRO994 polypeptide fused to a heterologous amino acid sequence. The PRO polypeptide is useful in pharmaceuticals, diagnostics, biosensors or bioreactors. It is particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TNF)- α from human blood, for stimulating the proliferation of pericyte cells, or stimulating the release of proteoglycans from cartilage. The polypeptide may be employed for a variety of therapeutic purposes, e.g. for treating cancer, wound healing, cartilage defects, osteoarthritis, rheumatoid arthritis. Also disclosed are the cDNA encoding PRO994, 83 other PRO polypeptides and their encoding cDNAs. The present sequence encodes a PRO polypeptide of the invention.

Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;

```
. Query Match      96.1%;   Score 998;   DB 7;   Length 998;
  Best Local Similarity 100.0%;   Pred. No. 0;
  Matches 998;   Conservative 0;   Mismatches 0;   Indels
```

Qy	14	CCGTTATCGCTTTCGCGCTACTGCTGTAATGTCCGTC	CGGAGGAGGAGGAGGCTTTTGC	73
Db	1	CCGTTATCGCTTTCGCGCTACTGCTGTAATGTCCGTC	CGGAGGAGGAGGCTTTTGC	60
Qy	74	CGCTGACCCAGAGATGGCCCCCGAGCGAGCAAAATTC	TACTGTCCGGTGTCCCGGCTACCG	133
Db	61	CGCTGACCCAGAGATGGCCCCCGAGCGAGCAAAATTC	TACTGTCCGGTGTCCCGGCTACCG	120
Qy	134	TGGCCGAGCTAGCAACCTTTCCCTTGGATCTCA	CAAAAACTCGACTCCAATTCGAGAG	193
Db	121	TGGCCGAGCTAGCAACCTTTCCCTTGGATCTCA	CAAAAACTCGACTCCAATTCGAGAG	180
Qy	194	AAGCAGCTCTTGTCTCGGTTGGGAGACGGTGC	CAAGAGAAATCGCCCCCTATAGGGGAAATGG	253
Db	181	AAGCAGCTCTTGTCTCGGTTGGGAGACGGTGC	CAAGAGAAATCTGCCCCCTATAGGGGAAATGG	240
Qy	254	TGGCCACAGCCCTAGGGATCAITTAAGAGAGAGGCTTT	TAAAGCTTTGGCAAGAGATGA	313
Db	241	TGGCCACAGCCCTAGGGATCAITTAAGAGAGAGGCTTT	TAAAGCTTTGGCAAGAGATGA	300
Qy	314	CACCCGCAATTTACAGACAGCTAGTGATTTCTG	GAGGTGCAATGGTCACATATGAACATC	373
Db	301	CACCCGCAATTTACAGACAGCTAGTGATTTCTG	GAGGTGCAATGGTCACATATGAACATC	360
Qy	374	TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAG	CAATATCCCTTTTGGAAATCAGTCA	433
Db	361	TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAG	CAATATCCCTTTTGGAAATCAGTCA	420
Qy	434	TTCGAGGATGATGGCTGGTGTTATTGGCCAGT	TTTTAGCCCAATCCAACTGACCTAGTGA	493
Db	421	TTGAGGGATGATGGCTGGTGTTATTGGCCAGT	TTTTAGCCCAATCCAACTGACCTAGTGA	480
Qy	494	AGGTTTCAGATGCAAAATGGAAGGAAAAAGGAAA	ACTGGAAGGAAAAACCAATTCGCATTTCTGT	553

Db 481 AGGTTTCAGATGCAAAATGGAAGGAAAGAAATGGAAGGAAACCAATTCGATTCGTG 540
 QY 554 GTGTACATCATGCTTTGCAAAATCTTACGTGAGAGGAGGAATACAGAGGCTTTGGGAG 613
 Db 541 GTGTACATCATGCTTTGCAAAATCTTACGTGAGAGGAGGAATACAGAGGCTTTGGGAG 600
 QY 614 GCTGGGTACCCCAATATACAAAGAGAGCACTGCTGAAATATGGAGATTTAACCCTTATG 673
 Db 601 GCTGGGTACCCCAATATACAAAGAGAGCACTGCTGAAATATGGAGATTTAACCCTTATG 660
 QY 674 ATACAGTGAACACACTACTTGGTATTTGAATACACCACTTTGAGGACAAATCATGACTCAAG 733
 Db 661 ATACAGTGAACACACTACTTGGTATTTGAATACACCACTTTGAGGACAAATCATGACTCAAG 720
 QY 734 GTTTATCAAGTTTATGTTCTGCACTGCTGAGTCTTCTTCTGGAACACACGCGGATGCA 793
 Db 721 GTTTATCAAGTTTATGTTCTGCACTGCTGAGTCTTCTTCTGGAACACACGCGGATGCA 780
 QY 794 TCAAAAGCAGAAATATGAATCAACACGAGATATAAAGGAGGAGCTTTTGTATTAAT 853
 Db 781 TCAAAAGCAGAAATATGAATCAACACGAGATATAAAGGAGGAGCTTTTGTATTAAT 840
 QY 854 CATCACTGACTGCTTGTATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAG 913
 Db 841 CATCACTGACTGCTTGTATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAG 900
 QY 914 GCTTTTACCCTTGGCTGAGATGACCCCTTGTCAATGCTTCTGCTTACTTATG 973
 Db 901 GCTTTTACCCTTGGCTGAGATGACCCCTTGTCAATGCTTCTGCTTACTTATG 960
 QY 974 AAAAAATCAGAGAGATGAGTGGAGTCACTGCTCAATTTAA 1011
 Db 961 AAAAAATCAGAGAGATGAGTGGAGTCACTGCTCAATTTAA 998

RESULT 14

ACA67333
 ID ACA67333 standard; cDNA; 998 BP.

ACA67333;

23-JUN-2003 (first entry)

cDNA encoding human secreted polypeptide PRO1566.

Human; Gene; ss; affinity purification.

Homo sapiens.

US2003027212-A1.

06-FEB-2003.

02-MAY-2002; 2002US-00063544.

30-DEC-1998; 98KR-00062142.

08-MAR-1999; 99WO-US005028.

14-MAY-1999; 99US-00311832.

25-AUG-1999; 99WO-US010733.

25-AUG-1999; 99US-00380137.

25-AUG-1999; 99US-00380138.

25-AUG-1999; 99US-00380139.

25-AUG-1999; 99US-00380142.

18-SEP-1999; 99US-00397342.

18-OCT-1999; 99US-00403297.

30-DEC-1999; 99US-00423844.

18-FEB-2000; 99WO-US031274.

PR 02-JUN-2000; 2000WO-US015264.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00815744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 29-JUN-2001; 2001US-00869599.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-DEC-2001; 2001US-00008867.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Eaton DL, Filvaroff B, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX
 DR WPI; 2003-341840/32.
 DR P-PSDB; AB081208.
 XX
 PT New monoclonal antibody that binds to a secreted and transmembrane
 PT polypeptide, useful for detecting and purifying the polypeptide and also
 PT for treating conditions responsive to the antibody.
 XX
 PS Example 4; Fig 125; 235pp; English.
 XX
 CC The invention relates to an antibody that binds to a secreted and
 CC transmembrane polypeptide, PRO1136. The antibody is useful for preparing
 CC a medicament useful in the treatment of a condition responsive to anti-
 CC PRO antibody. The antibody is also useful in diagnostic assays for PRO,
 CC by detecting its expression in specific cells, tissues or serum, and for
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. The present sequence represents a cDNA encoding a PRO
 CC polypeptide of the invention
 XX
 SQ Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;

Query Match 96.1%; Score 998; DB 7; Length 998;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCGTTATCGTCTTGCGTACTGCTGAATGTCGTCGCGGAGGAGGAGGAGGCTTTTGC 73
 Db 1 CCGTTATCGTCTTGCGTACTGCTGAATGTCGTCGCGGAGGAGGAGGAGGCTTTTGC 60
 QY 74 CGCTGACCCAGAGATGGCCCGCGGAGGAGCAAAATTCCTACTGTCGCGCTGCGGCTACCG 133
 Db 61 CGCTGACCCAGAGATGGCCCGCGGAGGAGCAAAATTCCTACTGTCGCGCTGCGGCTACCG 120
 QY 134 TGGCCGAGCTAGCAACCTTTCCCTGGATCTCACAAAACCTCGACTCCAAATGCAAGAG 193
 Db 121 TGGCCGAGCTAGCAACCTTTCCCTGGATCTCACAAAACCTCGACTCCAAATGCAAGAG 180
 QY 194 AAGCAGCTCTTCTCGGTTGGGAGACGGTGCAAGAGATCTGCCCTTATAGGGGAATGG 253
 Db 181 AAGCAGCTCTTCTCGGTTGGGAGACGGTGCAAGAGATCTGCCCTTATAGGGGAATGG 240
 QY 254 TGGCAGACGCCCTAGGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTGGCAAGAGTGA 313
 Db 241 TGGCAGACGCCCTAGGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTGGCAAGAGTGA 300
 QY 314 CACCGCCATTTCAGACAGCTAGTGTATTTCTGGAGTCCGAATGGTCCACATATGAACATC 373
 Db 301 CACCGCCATTTCAGACAGCTAGTGTATTTCTGGAGTCCGAATGGTCCACATATGAACATC 360

QY 374 TCCGAGAGGTTGTTGGTGGCAAGAGTGAAGATGAGCAATTATCCCTTTGGAATCAGTCA 433
 DB 361 TCCGAGAGGTTGTTGGTGGCAAGTGAAGATGAGCAATTATCCCTTTGGAATCAGTCA 420
 QY 434 TTGGAGGATGATGGCTGGTGGTATTGGCCAGTTTATGGCAATTCGAATCCTGAGTCTAGTGA 493
 DB 421 TTGGAGGATGATGGCTGGTGGTATTGGCCAGTTTATGGCAATTCGAATCCTGAGTCTAGTGA 480
 QY 494 AGGTTTCAGATGCAATTCGAAGGAAAGGAAAGTGAAGGAAAGCAATTCGGAATTCGTCG 553
 DB 481 AGGTTTCAGATGCAATTCGAAGGAAAGGAAAGTGAAGGAAAGCAATTCGGAATTCGTCG 540
 QY 554 GTGTACATCATGCTATTCGCAAAATCTTAGCTGAAGGAGGAATACAGAGGCTTTGGGCAG 613
 DB 541 GTGTACATCATGCTATTCGCAAAATCTTAGCTGAAGGAGGAATACAGAGGCTTTGGGCAG 600
 QY 614 GCTGGGTACCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 673
 DB 601 GCTGGGTACCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 660
 QY 674 ATACAGTGAACACTACTCTGTTATGAATACACCACTTGAGGACAAATATCATGACTCAG 733
 DB 661 ATACAGTGAACACTACTCTGTTATGAATACACCACTTGAGGACAAATATCATGACTCAG 720
 QY 734 GTTTATCAAGTTTATGTTCTGAGCTGGTAGCTTCTATTCTGGGAACACCAAGCCGATGTCA 793
 DB 721 GTTTATCAAGTTTATGTTCTGAGCTGGTAGCTTCTATTCTGGGAACACCAAGCCGATGTCA 780
 QY 794 TCAAAAGCAGAAATGAATCAACACGAGATAAACAAAGAGGGAGCTTTGTATTAAT 853
 DB 781 TCAAAAGCAGAAATGAATCAACACGAGATAAACAAAGAGGGAGCTTTGTATTAAT 840
 QY 854 CATCGACTGACTGCTGATTCAGCTGTTCAAGTGGAAGGATTCATGAGTCTATATAAG 913
 DB 841 CATCGACTGACTGCTGATTCAGCTGTTCAAGTGGAAGGATTCATGAGTCTATATAAG 900
 QY 914 GCTTTTATACCATCTTGGCTGAGATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 973
 DB 901 GCTTTTATACCATCTTGGCTGAGATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 960
 QY 974 AAAAAATCAGAGATGAGTGGAGTCACTGATTTAA 1011
 DB 961 AAAAAATCAGAGATGAGTGGAGTCACTGATTTAA 998
 RESULT 15
 ID ACH66306
 AC ACH66306;
 XX
 DT 14-OCT-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO1566 cDNA.
 XX
 KW Human; secreted and transmembrane protein; PRO; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003027986-A1.
 XX
 PD 06-FEB-2003.
 XX
 PF 02-MAY-2002; 2002US-00063549.
 XX
 PR 30-DEC-1998; 98KR-00062142.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.

PR 25-AUG-1999; 99US-00380142.
 PR 15-SEP-1999; 99US-00397342.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 30-DEC-1999; 99WO-US031274.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 29-JUN-2001; 2001US-00869599.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-DEC-2001; 2001US-00008667.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Eaton DL, Filyaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX
 DR WPI; 2003-456358/43.
 XX
 DR P-PSDB; AB053322.
 XX
 PT PRO polypeptide, useful for preparing a medicament for treating a
 condition associated with PRO polypeptide.
 XX
 PS Disclosure; Fig 125; 222pp; English.
 XX
 CC The invention describes an isolated polypeptide having at least 80, 85,
 CC 90, 95 or 99% identity with: (a) a sequence having 46-335 amino acids, or
 CC its extracellular domain; (b) a sequence having 46-335 amino acids,
 CC lacking its associated signal peptide; or (c) an amino acid sequence
 CC encoded by the full-length coding sequence of the cDNA (ATCC accession
 CC number 209956). The PRO (secreted and transmembrane) polypeptide is
 CC useful for preparing a medicament for treating a condition associated
 CC with PRO polypeptide. This sequence encodes a novel human secreted and
 CC transmembrane PRO polypeptide
 XX
 SQ Sequence 998 BP; 284 A; 202 C; 262 G; 250 T; 0 U; 0 Other;
 Query Match 96.1%; Score 998; DB 7; Length 998;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 CCGTTATCGTCTTGGCGTACTGCTGAATGTCCTCCCGGAGGAGGAGGAGGCTTTTGC 73
 DB 1 CCGTTATCGTCTTGGCGTACTGCTGAATGTCCTCCCGGAGGAGGAGGAGGCTTTTGC 60
 QY 74 CGCTGACCCAGAGATGGCCCGGAGGAGCAAAATTCCTACTGTCCGCTCGCGGCTACCG 133
 DB 61 CGCTGACCCAGAGATGGCCCGGAGGAGCAAAATTCCTACTGTCCGCTCGCGGCTACCG 120
 QY 134 TGGCCGAGCTAGCAACCTTTCCCTCGATCTCAAAAACTCGACTCCAAATCAAGGAG 193
 DB 121 TGGCCGAGCTAGCAACCTTTCCCTCGATCTCAAAAACTCGACTCCAAATCAAGGAG 180
 QY 194 AAGCAGCTCTTGTCTCGGTTGGGAGACGGTGCAGAGATCTGCCCTATAGGGAATGG 253

```

Db      |||||
181  AAGCAGCTCTGCTGGTTGGGAGACGGTGCAGAGAAATCTGCCCTATAGGGAATGG 240
QY      |||||
254  TGGGCACAGCCCTAGGGATCATTAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGAGTGA 313
Db      |||||
241  TGGGCACAGCCCTAGGGATCATTAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGAGTGA 300
QY      |||||
314  CACCCGCCATTTACAGACAGTAGTGTATTCTGGAGGTGGAATGCTACATATGAACATC 373
Db      |||||
301  CACCCGCCATTTACAGACAGTAGTGTATTCTGGAGGTGGAATGCTACATATGAACATC 360
QY      |||||
374  TCCGAGAGTGTGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAAATCAGTCA 433
Db      |||||
361  TCCGAGAGTGTGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAAATCAGTCA 420
QY      |||||
434  TTGGAGGGATGATGGCTGGTGTATTGGCCAGTTTTATAGCCAAATCCAACTAGTGA 493
Db      |||||
421  TTGGAGGGATGATGGCTGGTGTATTGGCCAGTTTTATAGCCAAATCCAACTAGTGA 480
QY      |||||
494  AGGTTTCAGATGCAATGGAAGGAAAGAACTGGAAGGAAACCAATTGGGATTTGGTG 553
Db      |||||
481  AGGTTTCAGATGCAATGGAAGGAAAGAACTGGAAGGAAACCAATTGGGATTTGGTG 540
QY      |||||
554  GTGTACATCATGCTTTGCAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAG 613
Db      |||||
541  GTGTACATCATGCTTTGCAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAG 600
QY      |||||
614  GCTGGGTACCCAAATACAAAGAGCAGCACCTGGTGAATATGGGAGATTTAACCACTTATG 673
Db      |||||
601  GCTGGGTACCCAAATACAAAGAGCAGCACCTGGTGAATATGGGAGATTTAACCACTTATG 660
QY      |||||
674  ATACAGTGAACACTACTTGGTATTGAATACACCACTTGAGGACAAATATCATGACTCACG 733
Db      |||||
661  ATACAGTGAACACTACTTGGTATTGAATACACCACTTGAGGACAAATATCATGACTCACG 720
QY      |||||
734  GTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAAACCCAGCCGATGCA 793
Db      |||||
721  GTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAAACCCAGCCGATGCA 780
QY      |||||
794  TCAAAAGCAGAAATATGAATCAACACGAGATAAACAAGGAGGGGACTTTTGTATAAAT 853
Db      |||||
781  TCAAAAGCAGAAATATGAATCAACACGAGATAAACAAGGAGGGGACTTTTGTATAAAT 840
QY      |||||
854  CATCGACTGACTGCTTGAATCAGGCTGTTCAAGTGAAGGATTCATGAGTCTATATAAG 913
Db      |||||
841  CATCGACTGACTGCTTGAATCAGGCTGTTCAAGTGAAGGATTCATGAGTCTATATAAG 900
QY      |||||
914  GCTTTTACCATCTTGGCTGAGATGACCCCTGGTCAATGGTCTTCTGGCTTACTTATG 973
Db      |||||
901  GCTTTTACCATCTTGGCTGAGATGACCCCTGGTCAATGGTCTTCTGGCTTACTTATG 960
QY      |||||
974  AAAAAATCAGAGATGAGTGGAGTCACTCAATTTAA 1011
Db      |||||
961  AAAAAATCAGAGATGAGTGGAGTCACTCAATTTAA 998

```

Search completed: September 24, 2004, 04:36:04
Job time : 458 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2004, 04:11:05 ; Search time 105 Seconds
(without alignments)
5491.371 Million cell updates/sec

Title: US-09-397-342C-2

Perfect score: 1039

Sequence: 1 cggagtcggtcccggttat.....cagatatccatcacactggc 1039

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	267.2	25.7	1696	4	US-09-833-381-806
2	93.4	9.0	876	4	US-09-501-558-1
3	79.6	7.7	936	4	US-09-743-847-1
4	78.4	7.5	1674	4	US-09-482-273-26
5	57.2	5.5	924	4	US-09-023-655-890
6	56.2	5.4	882	4	US-09-501-558-3
7	52.6	5.1	1430	4	US-09-489-847-39
8	50.8	4.9	1949	2	US-08-937-466-3
9	50.8	4.9	1949	3	US-09-172-528-3
10	50.8	4.9	1949	3	US-09-318-199-3
11	50.8	4.9	1949	3	US-09-503-579-3
12	49.4	4.8	930	4	US-10-001-051B-1
13	49.4	4.8	1255	1	US-08-518-878B-38
14	49.4	4.8	1255	1	US-08-294-522B-38
15	49.4	4.8	1255	1	US-08-470-868A-38
16	49.4	4.8	1596	2	US-08-807-861A-38
17	49.4	4.8	1596	2	US-09-210-681-38
18	49.4	4.8	1596	3	US-08-946-719A-38
19	49.4	4.8	1596	4	US-09-547-983-38
20	49.2	4.7	2782	2	US-08-937-466-1
21	49.2	4.7	2782	2	US-09-172-528-1
22	49.2	4.7	2782	2	US-09-318-199-1
23	49.2	4.7	2782	2	US-08-937-466-5
24	48.6	4.7	1777	2	US-09-172-528-5
25	48.6	4.7	1777	3	US-09-318-199-5
26	48.6	4.7	1777	3	US-09-503-579-5
27	48.6	4.7	1777	3	US-09-503-579-5

C	28	45.4	4.4	7218	1	US-08-232-463-14	Sequence 14, Appl
C	29	45	4.3	472	4	US-09-833-381-203	Sequence 203, App
C	30	37	3.6	1132	4	US-09-808-457-3	Sequence 3, Appli
C	31	37	3.6	1132	4	US-09-423-410-5	Sequence 5, Appli
C	32	37	3.6	1192	3	US-09-142-565-1	Sequence 1, Appli
C	33	37	3.6	1231	4	US-09-808-457-1	Sequence 1, Appli
C	34	37	3.6	1231	4	US-09-423-410-3	Sequence 3, Appli
C	35	35.2	3.4	62909	4	US-09-596-002-32	Sequence 32, Appl
C	36	34.2	3.3	3122	4	US-08-956-171B-519	Sequence 519, App
C	37	34	3.3	588	4	US-09-252-991A-13438	Sequence 13438, A
C	38	34	3.3	732	4	US-09-252-991A-13803	Sequence 13803, A
C	39	34	3.3	789	4	US-09-252-991A-13909	Sequence 13909, A
C	40	34	3.3	1205	1	US-08-518-878B-36	Sequence 36, Appl
C	41	34	3.3	1205	1	US-08-294-522B-37	Sequence 37, Appl
C	42	34	3.3	1205	2	US-08-807-861A-36	Sequence 36, Appl
C	43	34	3.3	1205	2	US-08-470-868A-36	Sequence 36, Appl
C	44	34	3.3	1205	3	US-09-210-681-36	Sequence 36, Appl
C	45	34	3.3	1205	3	US-08-946-719A-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-09-833-381-806
; Sequence 806, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-1119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 806
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-806

Query Match	25.7%	Score	267.2;	DB	4;	Length	1696;
Best Local Similarity	98.9%	Pred.	No. 3.2e-82;				
Matches	269;	Conservative	0;	Mismatches	3;	Indels	0;
						Gaps	0;
QY	332	ACGTAGTGTTCTTGGAGTTCGAATGGTGCACATATGAAACATCTCCGAGAGGTTGTGTTTG	391				
Db	1425	ACCCACTGTTATCTGGAGGTGCGAATGGTGCACATATGAAACATCTCCGAGAGGTTGTGTTTG	1484				
QY	392	GCAAAAGTCAGATGAGCATATCCCTTTGGAAATCAGTCATTTGGAGGATGATGCTG	451				
Db	1485	GCAAAAGTCAGATGAGCATATCCCTTTGGAAATCAGTCATTTGGAGGATGATGCTG	1544				
QY	452	GTGTTATTCGCCAGTTTGTAGCCAACTCCAACTAGTGAAGTTTCAGATCAAAATGG	511				
Db	1545	GTGTTATTCGCCAGTTTGTAGCCAACTCCAACTAGTGAAGTTTCAGATCAAAATGG	1604				
QY	512	AAGGAAAAAGGAAACTGGAAGGAAAAACCATTCGATTTTGGTGTGTACATCATGCAATTTG	571				
Db	1605	AAGGAAAAAGGAAACTGGAAGGAAAAACCATTCGATTTTGGTGTGTACATCATGCAATTTG	1664				
QY	572	CAAAATCTTAGCTGAAGGAGGATACGAGGG	603				
Db	1665	CAAAATCTTAGCTGAAGGAGGATACGAGGG	1696				

RESULT 2
US-09-501-558-1
; Sequence 1, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:

4

[illegible]

268	Db	TACCAGAGCTTGAAGCGACTATTCA TTGAAGCCCAAGATG-----AAACTCTACCG	321
424	Qy	AAATCAGTCATTGGAGGATGATGCGTGTGTTATTGGCCAGTTTTAGCCAATCAACT	483
322	Db	ATAAATGTGATGTGGAAATCTGCTGGAGTCATCTCTTAACCAATTGCTTAATCCAAC	381
484	Qy	GACCTAGTGAAGGTTTCAGATGCMAATGGAAGGAAAAAGGAAACTTGAAGGAAAAACCATTTG	543
382	Db	GATGTTTTGAAAATTCGGATGCAAGCGCAAGCAACACCATTC AAGGAGAA-----	433
544	Qy	CGATTCGTGGTGTACATCATGCAATTCGAAAACTTAGCTGAAGGAGGAATACGAGG	603
434	Db	-----TGATAGGCAACTTCATG-----AACATTTACCAACAAGAGGGGCAAGAGGA	480
604	Qy	CTTTGGGAGGCTGGGTACCCAAATATACAAGAGAGCACTGGTGAATATGGGAGATTTA	663
481	Db	CTGTGAAGGGTGTGCCCTTACTGGGACAGGGCTGCTATTGTTGTTGGTGTGGAGCTG	540
664	Qy	ACCACCTATGTATACAGTGAACACACTATTGGTATTGAATACACCACTTGAGGACAAATATC	723
541	Db	CCGGTCTATGACATCACCAAGAAGCATCTTATCTCTCAGGCCCTGATGGAGACACTGTG	600
724	Qy	ATGACTCAGGGTTATCAAGTTTATGTTCTCGACTGGTAGCTTCTATTCTTCGGGAACA	783
601	Db	TATACCACCTTCCTCTCAAGCTTCACCTGTGTGCTCGCAGGGGGCCCTGGCCCTCAAA	660
784	Qy	GCCGATGTCATCAAGAAGAGTAATGTGAATCAACCAAGAGTAATACAGAGAGGGGAC	843

```

661 GTTGATGTTGTGAGCACGCTAAGTAAGTAATCAGAGAGTGCTTCGAGATGGCAGATGTTCT 720
      |||
844 TTGTAATAATCATCGACTGACTGCTTGTTGATTCAG 876
      |||
721 GGCTACACAGGAACCCCTGGATTGCTTGTTCAG 753
      |||

RESULT 7
US-09-489-847-39
; Sequence 39, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZO31P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30

```

EARLIER APPLICATION NUMBER: 60/095,486
 EARLIER FILING DATE: 1998-08-05
 EARLIER APPLICATION NUMBER: 60/096,319
 EARLIER FILING DATE: 1998-08-12
 EARLIER APPLICATION NUMBER: 60/095,454
 EARLIER FILING DATE: 1998-08-06
 EARLIER APPLICATION NUMBER: 60/095,455
 EARLIER FILING DATE: 1998-08-06
 NUMBER OF SEQ ID NOS: 376
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 39
 LENGTH: 1430
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-489-847-39

Query Match 5.1%; Score 52.6; DB 4; Length 1430;
 Best Local Similarity 50.1%; Pred. No. 1.6e-07;
 Matches 201; Conservative 0; Mismatches 179; Indels 21; Gaps 2;
 QY 117 CGGCTGCGCGCTACCGTGGCGGAGCTAGCAACCTTTCCCTCGATCTCAAAAACCTCG 176
 DB 328 CGGCTTGCCTCTATCTGCTGCTAGTTTGGACTTTCCCTGCGACCTTACCAAAACAG 387
 QY 177 ACTCCAAATCAAGGAGAACAGCTCTTGTCTCGTTGGGAGACGGTGCAGAGAAATCTGC 236
 DB 388 ACTTCAGTTCAAGGCCAAAGCATTGATGCCGTTTCAAAGAGATAAAA-----436
 QY 237 CCCTATAGGGGAATGTTGGCGCACAGCCCTAGGGATCAITGAAGAGGAAGCTTCTAAA 296
 DB 437 ----TATAGAGGATGTTTCCATCGCTGTTTCCCATCTCTAAAGAGGAAGGTGTTATGGC 492
 QY 297 GCTTTGGCAAGGAGTAGACCCGCCATTTACAGACAGTAGTGTATTCTGGAGGTGGAAT 356
 DB 493 TCTCTATTAGGAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552
 QY 357 GGTCAATATGAACATCTCCGAGAGGTGTTGTTGGCAAAAGTGAAGATGAGCATTATCC 416
 DB 553 TGGGATTTACAAAGCTTGAAGCGCTTATTTCGTAGAACGTTTAGAAGATGAAACT-----607
 QY 417 CTTTGGMAATCAGTCAATTGGAGGATGATGGCTGTTGTTATTTGGCCAGTTTTTAGCCAA 476
 DB 608 -CTTTTAAATTAATGATGCTGTGGGGTAGTGTGAGGAGTGATATCTTCCACTATAGCCAA 666
 QY 477 TCCAACTGACCTAGTGAAGGTTTCAGATGCAAAATGGAAGGAA 517
 DB 667 TCCACCGATGTTCTAAGATTTCGATGCAAGGCTCAGGAA 707

RESULT 8
 US-08-937-466-3
 ; Sequence 3, Application US/08937466
 ; Patent No. 5846779
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Ning
 ; APPLICANT: Amaral, M. Catherine
 ; APPLICANT: Chen, Jin-Long
 ; TITLE OF INVENTION: UCP3 Genes
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 75 DENISE DRIVE
 ; CITY: HILLSBOROUGH
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94010
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/937,466

FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A.
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-009
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 343-4341
 TELEFAX: (650) 343-4342
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1949 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-937-466-3
 Query Match 4.9%; Score 50.8; DB 2; Length 1949;
 Best Local Similarity 47.6%; Pred. No. 8.6e-07;
 Matches 200; Conservative 0; Mismatches 202; Indels 18; Gaps 1;
 QY 563 ATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATACAGGGCTTTGGGAGGCTGGGTAC 622
 DB 718 ATGCCTACAGAACCATCGCCAGGAGGAAGAGTCAAGGGCCCTGTGGAAAGGACTTTGGC 777
 QY 623 CCAATATACAAAGACGACGACTGTTGAATATGGAGATTAAACCACTTATGATACAGTGA 682
 DB 778 CCAACATACAGAAATGCCATTTGCTCACTGCTGAGATGGTACCTACGACATCATCA 837
 QY 683 AACACTACTTGTGTTGAATATACCACTTTGAGGACAAATATCATGACTCACGGTTTATCAA 742
 DB 838 AGGAGAAGTTGCTGGAGTCTCACTGTTTACTGACAACTTCCCTGTCACCTTTGTCTCTG 897
 QY 743 GTTATGTTCTGACTGTTGAGTCTTCTTCTGGAACACAGCGGATGTCATCAAAAGCA 802
 DB 898 CTTTGGAGCTGCTTCTGTGCCACAGTGTGGCTCCCGGGTGGATGTGTTAAAGACCC 957
 QY 803 GAATAATGAATCAACACGAGATAAACAAGGAAGGGAGCTTTTGTATATAATCATCGACTG 862
 DB 958 GATACATGAACGCTCCCTAGGAGGTACCGACGCCCTCTGC-----999
 QY 863 ACTGCTTGAATTCAGGCTGTTTCAAGGTGAAGGATTCATGAGTCTATATATAAAGGCTTTTAC 922
 DB 1000 ACTGTATGCTGAAGATGGTGGCTCAGGAGGACCCACGGCTTCTACAAAGGATTTCTGC 1059
 QY 923 CATCTTGGCTGAGAATGACCCCTTGGTCAATGTTGTTCTGCTTACTTATGAAAAATCA 982
 DB 1060 CCTCCTTTCTGCTGCTGGAGCTTGGAAACGTGATGATGTTTGTAAACATATGAGCACTGA 1119

RESULT 9
 US-09-172-528-3
 ; Sequence 3, Application US/09172528
 ; Patent No. 5952469
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Ning
 ; APPLICANT: Amaral, M. Catherine
 ; APPLICANT: Chen, Jin-Long
 ; TITLE OF INVENTION: UCP3 Genes
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 75 DENISE DRIVE
 ; CITY: HILLSBOROUGH
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94010
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/172,528
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,466
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1949 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-172-528-3

Query Match 4.9%; Score 50.8; DB 2; Length 1949;
Best Local Similarity 47.6%; Pred. No. 8.6e-07;
Matches 200; Conservative 0; Mismatches 202; Indels 18; Gaps 1;

QY 563 ATGCATTTGCAAAATCTTAGCTGAGGAGGAATACGAGGCTTTGGCAGGCTGGGTAC 622
Db 718 ATGCCTACAGAACCATCCCGAGGAGGAAGAGTCAGGGGCTGTGGAAAGGACTTGGC 777
QY 623 CCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAACCACTTATGATACAGTGA 682
Db 778 CCAACATCACAGAAATCCCAATTGTCACTGTGTGATGTGACCTACCAATCATCA 837
QY 683 AACACTATTGGTATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAA 742
Db 838 AGGAGAAGTCTGTGGAGTCTCACCTGTTTACTGACAACTTCCCTGTCTCTG 897
QY 743 GTTTATGTTCTGGACTGTGACTCTTCTATCTCGGACACCAAGGAGGACATCAAAAGCA 802
Db 898 CCTTGGAGCTGGCTTCTGTGCCACAGTGTGGCTCCCGGTGGATGTGTAAGACCC 957
QY 803 GAATAATGAATCAACACGAGATAAACAAGAGGAGGACATTTTGTATAAATCATCGACTG 862
Db 958 GATACATGAACGCTCCCTAGGAGTACCGGAGCCCTCTGC----- 999
QY 863 ACTGCTTGATTCAGCTGTTCAAGGTGAAGATTTCATGATCTATATAAAGGCTTTTAC 922
Db 1000 ACTGTATGCTGAAGATGGTGGCTCAGGAGGAGCCACGCGGCTTCTACAAAGGATTTGTC 1059
QY 923 CATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTCGCTTACTTATGAAAATCA 982
Db 1060 CCTCTTCTGCTGGAGCTTGGAACTGATGATGTTGTAAACATATGAGCAACTGA 1119

RESULT 10
US-09-318-199-3
; Sequence 3, Application US/09318199
; Patent No. 6025469
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ning
; APPLICANT: Amaral, M. Catherine
; APPLICANT: Chen, Jin-Long
; TITLE OF INVENTION: UCP3 Genes
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
```

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/318,199
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,466
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1949 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-318-199-3

Query Match 4.9%; Score 50.8; DB 3; Length 1949;
Best Local Similarity 47.6%; Pred. No. 8.6e-07;
Matches 200; Conservative 0; Mismatches 202; Indels 18; Gaps 1;

QY 563 ATGCATTTGCAAAATCTTAGCTGAAAGGAGGAATACAGAGGCTTTGGCAGGCTGGGTAC 622
Db 718 ATGCCTACAGAACCATCCCGAGGAGGAAGAGTCAGGGGCTGTGGAAAGGACTTGGC 777
QY 623 CCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAACCACTTATGATACAGTGA 682
Db 778 CCAACATCACAGAAATGCCATTGTCACTGTGTGATGTGACCTACGACATCATCA 837
QY 683 AACACTACTTGGTATTGAATACACCACTTTGAGGACAATATCATGACTCACGGTTTATCAA 742
Db 838 AGGAGAAGTCTGTGGAGTCTCACCTGTTTACTGACAACTTCCCTGTCTCTG 897
QY 743 GTTTATGTTCTGGACTGTGAGTCTTCTATCTCGGAAACACAGCGGATGTCATAAAGCA 802
Db 898 CCTTGGAGCTGGCTTCTGTGCCACAGTGTGGCTCCCGGTGGATGTGTAAGACCC 957
QY 803 GAATAATGAATCAACACGAGATAAACAAGAGGAGGACATTTTGTATAAATCATCGACTG 862
Db 958 GATACATGAACGCTCCCTAGGAGTACCGGAGCCCTCTGC----- 999
QY 863 ACTGCTTGATTCAGGCTGTTCAAGGTGAAGATTTCATGATCTATATAAAGGCTTTTAC 922
Db 1000 ACTGTATGCTGAAGATGGTGGCTCAGGAGGAGCCACGCGGCTTCTACAAAGGATTTGTC 1059
QY 923 CATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTCGCTTACTTATGAAAATCA 982
Db 1060 CCTCTTCTGCTGGAGCTTGGAACTGATGATGTTGTAAACATATGAGCAACTGA 1119

RESULT 11
US-09-503-579-3
; Sequence 3, Application US/09503579
; Patent No. 6248561
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ning
; APPLICANT: Amaral, M. Catherine
; APPLICANT: Chen, Jin-Long
; TITLE OF INVENTION: UCP3 Genes
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
```


STREET: 75 DENISE DRIVE
 CITY: HILLSBOROUGH
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94010
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/09/503,579
 APPLICATION NUMBER: US/09/503,579
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/937,466
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-009
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 343-4341
 TELEFAX: (650) 343-4342
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1949 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-503-579-3

Query Match 4.8%; Score 50.8; DB 3; Length 1949;
 Best Local Similarity 47.6%; Pred. No. 8.6e-07;
 Matches 200; Conservative 0; Mismatches 202; Indels 18; Gaps 1;
 QY 563 ATGCATTTCGAAAAATCTTAGCTGAAGGAGGAATACAGAGGCTTTGGGACGGCTGGGTAC 622
 DB 718 ATGCCTACAGAACCATCGCCAGGAGGAGAGGTACAGGCGCTTGTGGAAGGAGCTTGGC 777
 QY 623 CCAATATACAAAGACGACGACTGGTGAATATGGAGATTTAAACACTTATGATACAGTGA 682
 DB 778 CCAACATACAGAAATGCCATTGTCAACTGTGTGATGATGGTGACCTACGACATCATCA 837
 QY 683 AACACTACTTGGTATTGAATACACCACTTCAGGACATATCATGACTCAGGTTTATCAA 742
 DB 838 AGGAGAAGTTGCTGGAGTCTCACCTGTCTTACTGACAACTTCCCTGTCTCTG 897
 QY 743 GTTTATGTTCTGACTGGTAGCTTCTATTCTGGGAACACCCAGCGGATGTCATCAAAAGCA 802
 DB 898 CCTTTGGAGTGGCTTCTGTGCCACAGTGTGGCTCCCGGTGGATGGTAAAGACC 957
 QY 803 GAATAATGAATCAACCAAGAGATAAACAAGGAAGGGGACTTTTGTATATAATCATCGACTG 862
 DB 958 GATACATGAACGCTCCCTAGGAGGTACCGAGCCCTCTGC----- 999
 QY 863 ACTGCTTGATTCAGGCTGTTCAAGGTGAAGGATTCATGACTCTATATAAGGCTTTTAC 922
 DB 1000 ACTGTATGCTGAAGATGGTGGCTCAGGAGGAGGCCACGCGCTTCTACAAAGGATTTGTGC 1059
 QY 923 CATCTTGGCTGAGAAAGACCCCTTGGTCAATGTTGTTCTGGCTTACTTATGAAAAAATCA 982
 DB 1060 CCTCCTTTCTGCTCTGGGAGCTTGGACGTGATGATGTTGTAAACATATGACCAACTGA 1119

RESULT 12
 US-10-001-051B-1
 ; Sequence 1, Application US/10001051B
 ; Patent No. 6670138
 ; GENERAL INFORMATION:
 ; APPLICANT: Gonzalez-Zulueta, Mirella
 ; APPLICANT: Shamloo, Mehrdad

APPLICANT: McFarland, K.C.
 APPLICANT: Chin, Daniel
 APPLICANT: Wieloch, Tadeusz
 APPLICANT: Melcher, Thorsten
 APPLICANT: AGY Therapeutics, Inc.
 TITLE OF INVENTION: METHODS OF DIAGNOSING , PREVENTING AND TREATING
 FILE REFERENCE: NEUROLOGICAL DISORDERS AND NEURONAL INJURIES
 CURRENT APPLICATION NUMBER: US/10/001,051B
 CURRENT FILING DATE: 2002-06-25
 PRIOR APPLICATION NUMBER: US 60/244,946
 PRIOR FILING DATE: 2000-11-01
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 930
 TYPE: DNA
 ORGANISM: Unknown Organism
 FEATURE:
 OTHER INFORMATION: Description of Unknown Organism: Any animal
 OTHER INFORMATION: source, typically mammalian, most typically human
 US-10-001-051B-1

Query Match 4.8%; Score 49.4; DB 4; Length 930;
 Best Local Similarity 49.1%; Pred. No. 1.1e-06;
 Matches 199; Conservative 0; Mismatches 191; Indels 15; Gaps 2;
 QY 103 AAATTCCTACTGTCGGCTGCGCGCTACCGTACCGTCCGCGAGGTAGCAACCTTTCCCTCGAT 162
 DB 46 AAGTTTCTTGGGGCTGGCACAGCTGCTGCATCGCAGATCTCATCACCCTTTCTCTCGAT 105
 QY 163 CTCACAAAAAATCGACTCCAAATGCAAGGAGAGAGAGCTCTTGCTCGTTGGGAGACGGT 222
 DB 106 ACTGCTAAGTCCGGTTACAGATCCAGAGGAAAG-----TCAGGGGCCAGTGGC 156
 QY 223 GCAAGAGAATTCGCCCTTATAGGGAATGGTGGCAGAGCCCTTAGGATCATTTGAAGAG 282
 DB 157 GCTACAGCAGCGCCAGTACCGCGTGTGATGGCAGCATTCTGACCATGTCGCGTACT 216
 QY 283 GAAGGCTTCTTAAGCTTTGGCAAGAGTGCACACCGCCATTTACAGACAGTGTAT 342
 DB 217 GAGGGCCCCGAGAGCCTCTACAATGGGTGTTGCGCGCTCGAGGCCCAATGAGCTTT 276
 QY 343 TCTGGAGGTGCAATGGTTCACATATGAACATCTCCGAGAGGTGTGTTTGGCAAAAGTGA 402
 DB 277 GCCTCTGTCGGATCGGCTGTATGATTCGTCAACA-----GTCTACCAAGGGC 330
 QY 403 GATGACATATCCCTTTGGAAATCAGTCAATGGAGGAGATGCGTGTGTATTGGC 462
 DB 331 TCTGAGCATGCCAGCATTTGGAGCGCTCTCTAGCAGGAGCAGCAGGTGCGCTGCT 390
 QY 463 CAGTTTTTAGCCANTCCAATGACCTAGTGAAGTTTCAGATGCAA 507
 DB 391 GTGGCTGTGGCCCGACCCACGGATGTGTAAGGTCGGATTCGATTCCAA 435

RESULT 13
 US-08-518-878B-38
 ; Sequence 38, Application US/08518878B
 ; Patent No. 5702902
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:


```

, MEDIUM TYPE: Floppy disk
,
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: Patent In Release #1.0, Version #1.30
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/470,868A
, FILING DATE: 06-JUN-1995
, CLASSIFICATION: 530
, ATTORNEY/AGENT INFORMATION:
, NAME: Coruzzi, Laura A.
, REGISTRATION NUMBER: 30,742
, REFERENCE/DOCKET NUMBER: 7853-0031-999
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (212) 790-9090
, TELEFAX: (212) 869-8864
, TELEX: 66441 PENNIE
, INFORMATION FOR SEQ ID NO: 39:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 1255 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, US-08-470-868A-38

```

Query Match	4.8%;	Score 49.4;	DB 2;	Length 1255;
Best Local Similarity	49.1%;	Pred. No. 1.9e-06;		
Matches 199;	Conservative 0;	Mismatches 191;	Indels 15;	Gaps 2;
QY	103	AAATTCCTACTGTCGGGCTGCGGGCTACCGTGGCGGAGCTAGCAACCTTTCCCTCGAT	162	
Db	16	AAGTTTCCTGGGCTGGCACAGCTGCCTGCATCGCAGATCTCATCACTTCTCTCTGAT	75	
QY	163	CTCACAAAACTCGACTCCAAATCAAGGAGAACGAGCTCTTGCTCGGTTGGGAGACGGT	222	
Db	76	ACTGCTAAAGTCGGTTACAGATCCAAAGGAGAAAG-----TCAGGGGCCAGTGC	126	
QY	223	GCAAGAGAACTCGCCCCCTATAGGGGAATGGTGGCGCACAGCCCTAGGGATCATTTGAAGAG	282	
Db	127	GCTACAGTCAGCGCCCAAGTACCGCGGTGTGATGGGCACCAATTCATGACCATGGTCGGTACT	186	
QY	283	GAAGGCTTTTCTAAAGCTTTGGCAAGGAGTGCACACCCGCCAATTTACAGACAGCTAGTGAT	342	
Db	187	GAGGGCCCCGGAAGCCTCTCAATGGGCTGTTGCCGCGCTGCAGCGCCAAATGAGCTTT	246	
QY	343	CTTGGAGGTGCAATGGTGCATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAA	402	
Db	247	GCCTCTGTCCGCATCGGCCCTGTATGATTTCTGTCAACA-----GTTCTACACCAAGGCG	300	
QY	403	GATTGAGCATTATCCCCCTTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTATGGC	462	
Db	301	TCTGAGCATGCCAGCATTGGGAGCGCGCTCTTAGCAGGCGACCAACAGGTGCCCTGCT	360	
QY	463	CAGTTTTTAGCCCAATCCAACTGACCTAGTGAAGGTTCAGATGCAA	507	
Db	361	GTGGCTGTGGCCACAGCCACCGGATGTGGTAAAGGTCGGATTTCCAA	405	

Search completed: September 24, 2004, 06:30:54
Job time : 109 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2004, 05:44:43 ; Search time 3500 Seconds
(without alignments)

1503.566 Million cell updates/sec

Title: US-09-397-342C-2

Perfect score: 1039

Sequence: 1 ccgagctcgatcccgcttat.....cagatcatcatcacactggc 1039

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3337386 seqs, 2532474682 residues

Total number of hits satisfying chosen parameters: 6674772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	998	96.1	998	10	US-09-946-374-405 Sequence 405, App
2	998	96.1	998	12	US-10-015-395A-405 Sequence 405, App
3	998	96.1	998	13	US-10-063-745-125 Sequence 125, App
4	998	96.1	998	13	US-10-063-513-125 Sequence 125, App
5	998	96.1	998	13	US-10-063-513-125 Sequence 125, App
6	998	96.1	998	13	US-10-063-569-125 Sequence 125, App
7	998	96.1	998	13	US-10-063-551-125 Sequence 125, App
8	998	96.1	998	13	US-10-006-485A-405 Sequence 405, App
9	998	96.1	998	13	US-10-013-907A-405 Sequence 405, App
10	998	96.1	998	13	US-10-015-499A-405 Sequence 405, App
11	998	96.1	998	13	US-10-063-555-125 Sequence 125, App
12	998	96.1	998	13	US-10-063-563-125 Sequence 125, App
13	998	96.1	998	13	US-10-063-594-125 Sequence 125, App
14	998	96.1	998	13	US-10-063-553-125 Sequence 125, App

15	998	96.1	998	13	US-10-063-554-125	Sequence 125, App
16	998	96.1	998	13	US-10-226-254A-405	Sequence 405, App
17	998	96.1	998	14	US-10-006-867-125	Sequence 125, App
18	998	96.1	998	14	US-10-063-547-125	Sequence 125, App
19	998	96.1	998	15	US-10-063-616-125	Sequence 125, App
20	998	96.1	998	15	US-10-063-502-125	Sequence 125, App
21	998	96.1	998	15	US-10-006-858A-405	Sequence 405, App
22	998	96.1	998	15	US-10-063-518-125	Sequence 125, App
23	998	96.1	998	15	US-10-063-598-125	Sequence 125, App
24	998	96.1	998	15	US-10-227-693-125	Sequence 125, App
25	998	96.1	998	15	US-10-006-818A-405	Sequence 405, App
26	998	96.1	998	15	US-10-015-393A-405	Sequence 405, App
27	998	96.1	998	15	US-10-063-567-125	Sequence 125, App
28	998	96.1	998	15	US-10-015-869A-405	Sequence 405, App
29	998	96.1	998	15	US-10-012-121A-405	Sequence 405, App
30	998	96.1	998	15	US-10-063-599-125	Sequence 125, App
31	998	96.1	998	15	US-10-006-116A-405	Sequence 405, App
32	998	96.1	998	15	US-10-006-117A-405	Sequence 405, App
33	998	96.1	998	15	US-10-017-527A-405	Sequence 405, App
34	998	96.1	998	15	US-10-013-913A-405	Sequence 405, App
35	998	96.1	998	15	US-10-063-595-125	Sequence 125, App
36	998	96.1	998	15	US-10-007-194A-405	Sequence 405, App
37	998	96.1	998	15	US-10-013-430A-405	Sequence 405, App
38	998	96.1	998	15	US-10-011-671A-405	Sequence 405, App
39	998	96.1	998	15	US-10-012-753A-405	Sequence 405, App
40	998	96.1	998	15	US-10-015-386A-405	Sequence 405, App
41	998	96.1	998	15	US-10-063-580-125	Sequence 125, App
42	998	96.1	998	15	US-10-011-692A-405	Sequence 405, App
43	998	96.1	998	15	US-10-063-557-125	Sequence 125, App
44	998	96.1	998	15	US-10-006-768A-405	Sequence 405, App
45	998	96.1	998	15	US-10-017-610A-405	Sequence 405, App

ALIGNMENTS

RESULT 1

US-09-946-374-405
; Sequence 405, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01

1 ; PRIOR APPLICATION NUMBER: 60/098750
2 ; PRIOR FILING DATE: 1998-09-01
3 ; PRIOR APPLICATION NUMBER: 60/098803
4 ; PRIOR FILING DATE: 1998-09-02
5 ; PRIOR APPLICATION NUMBER: 60/098821
6 ; PRIOR FILING DATE: 1998-09-02
7 ; PRIOR APPLICATION NUMBER: 60/098843
8 ; PRIOR FILING DATE: 1998-09-02
9 ; PRIOR APPLICATION NUMBER: 60/099536
10 ; PRIOR FILING DATE: 1998-09-09
11 ; PRIOR APPLICATION NUMBER: 60/099596
12 ; PRIOR FILING DATE: 1998-09-09
13 ; PRIOR APPLICATION NUMBER: 60/099598
14 ; PRIOR FILING DATE: 1998-09-09
15 ; PRIOR APPLICATION NUMBER: 60/099602
16 ; PRIOR FILING DATE: 1998-09-09
17 ; PRIOR APPLICATION NUMBER: 60/099642
18 ; PRIOR FILING DATE: 1998-09-09
19 ; PRIOR APPLICATION NUMBER: 60/099741
20 ; PRIOR FILING DATE: 1998-09-10
21 ; PRIOR APPLICATION NUMBER: 60/099754
22 ; PRIOR FILING DATE: 1998-09-10
23 ; PRIOR APPLICATION NUMBER: 60/099763
24 ; PRIOR FILING DATE: 1998-09-10
25 ; PRIOR APPLICATION NUMBER: 60/099792
26 ; PRIOR FILING DATE: 1998-09-10
27 ; PRIOR APPLICATION NUMBER: 60/099808
28 ; PRIOR FILING DATE: 1998-09-10
29 ; PRIOR APPLICATION NUMBER: 60/099812
30 ; PRIOR FILING DATE: 1998-09-10
31 ; PRIOR APPLICATION NUMBER: 60/099815
32 ; PRIOR FILING DATE: 1998-09-10
33 ; PRIOR APPLICATION NUMBER: 60/099816
34 ; PRIOR FILING DATE: 1998-09-10
35 ; PRIOR APPLICATION NUMBER: 60/100385
36 ; PRIOR FILING DATE: 1998-09-15
37 ; PRIOR APPLICATION NUMBER: 60/100388
38 ; PRIOR FILING DATE: 1998-09-15
39 ; PRIOR APPLICATION NUMBER: 60/100390
40 ; PRIOR FILING DATE: 1998-09-15
41 ; PRIOR APPLICATION NUMBER: 60/100584
42 ; PRIOR FILING DATE: 1998-09-16
43 ; PRIOR APPLICATION NUMBER: 60/100627
44 ; PRIOR FILING DATE: 1998-09-16
45 ; PRIOR APPLICATION NUMBER: 60/100661
46 ; PRIOR FILING DATE: 1998-09-16
47 ; PRIOR APPLICATION NUMBER: 60/100662
48 ; PRIOR FILING DATE: 1998-09-16
49 ; PRIOR APPLICATION NUMBER: 60/100664
50 ; PRIOR FILING DATE: 1998-09-16
51 ; PRIOR APPLICATION NUMBER: 60/100683
52 ; PRIOR FILING DATE: 1998-09-17
53 ; PRIOR APPLICATION NUMBER: 60/100684
54 ; PRIOR FILING DATE: 1998-09-17
55 ; PRIOR APPLICATION NUMBER: 60/100710
56 ; PRIOR FILING DATE: 1998-09-17
57 ; PRIOR APPLICATION NUMBER: 60/100711
58 ; PRIOR FILING DATE: 1998-09-17
59 ; PRIOR APPLICATION NUMBER: 60/100848
60 ; PRIOR FILING DATE: 1998-09-18
61 ; PRIOR APPLICATION NUMBER: 60/100849
62 ; PRIOR FILING DATE: 1998-09-18
63 ; PRIOR APPLICATION NUMBER: 60/100919
64 ; PRIOR FILING DATE: 1998-09-17
65 ; PRIOR APPLICATION NUMBER: 60/100930
66 ; PRIOR FILING DATE: 1998-09-17
67 ; PRIOR APPLICATION NUMBER: 60/101014
68 ; PRIOR FILING DATE: 1998-09-18
69 ; PRIOR APPLICATION NUMBER: 60/101068
70 ; PRIOR FILING DATE: 1998-09-18
71 ; PRIOR APPLICATION NUMBER: 60/101071
72 ; PRIOR FILING DATE: 1998-09-18
73 ; PRIOR APPLICATION NUMBER: 60/101279

1 ; PRIOR FILING DATE: 1998-09-22
2 ; PRIOR APPLICATION NUMBER: 60/101471
3 ; PRIOR FILING DATE: 1998-09-23
4 ; PRIOR APPLICATION NUMBER: 60/101472
5 ; PRIOR FILING DATE: 1998-09-23
6 ; PRIOR APPLICATION NUMBER: 60/101474
7 ; PRIOR FILING DATE: 1998-09-23
8 ; PRIOR APPLICATION NUMBER: 60/101475
9 ; PRIOR FILING DATE: 1998-09-23
10 ; PRIOR APPLICATION NUMBER: 60/101476
11 ; PRIOR FILING DATE: 1998-09-23
12 ; PRIOR APPLICATION NUMBER: 60/101477
13 ; PRIOR FILING DATE: 1998-09-23
14 ; PRIOR APPLICATION NUMBER: 60/101479
15 ; PRIOR FILING DATE: 1998-09-23
16 ; PRIOR APPLICATION NUMBER: 60/101738
17 ; PRIOR FILING DATE: 1998-09-24
18 ; PRIOR APPLICATION NUMBER: 60/101741
19 ; PRIOR FILING DATE: 1998-09-24
20 ; PRIOR APPLICATION NUMBER: 60/101743
21 ; PRIOR FILING DATE: 1998-09-24
22 ; PRIOR APPLICATION NUMBER: 60/101915
23 ; PRIOR FILING DATE: 1998-09-24
24 ; PRIOR APPLICATION NUMBER: 60/101916
25 ; PRIOR FILING DATE: 1998-09-24
26 ; PRIOR APPLICATION NUMBER: 60/102207
27 ; PRIOR FILING DATE: 1998-09-29
28 ; PRIOR APPLICATION NUMBER: 60/102240
29 ; PRIOR FILING DATE: 1998-09-29
30 ; PRIOR APPLICATION NUMBER: 60/102307
31 ; PRIOR FILING DATE: 1998-09-29
32 ; PRIOR APPLICATION NUMBER: 60/102330
33 ; PRIOR FILING DATE: 1998-09-29
34 ; PRIOR APPLICATION NUMBER: 60/102331
35 ; PRIOR FILING DATE: 1998-09-29
36 ; PRIOR APPLICATION NUMBER: 60/102484
37 ; PRIOR FILING DATE: 1998-09-30
38 ; PRIOR APPLICATION NUMBER: 60/102487
39 ; PRIOR FILING DATE: 1998-09-30
40 ; PRIOR APPLICATION NUMBER: 60/102570
41 ; PRIOR FILING DATE: 1998-09-30
42 ; PRIOR APPLICATION NUMBER: 60/102571
43 ; PRIOR FILING DATE: 1998-09-30
44 ; PRIOR APPLICATION NUMBER: 60/102684
45 ; PRIOR FILING DATE: 1998-10-01
46 ; PRIOR APPLICATION NUMBER: 60/102687
47 ; PRIOR FILING DATE: 1998-10-01
48 ; PRIOR APPLICATION NUMBER: 60/102965
49 ; PRIOR FILING DATE: 1998-10-02
50 ; PRIOR APPLICATION NUMBER: 60/103258
51 ; PRIOR FILING DATE: 1998-10-06
52 ; PRIOR APPLICATION NUMBER: 60/103314
53 ; PRIOR FILING DATE: 1998-10-07
54 ; PRIOR APPLICATION NUMBER: 60/103315
55 ; PRIOR FILING DATE: 1998-10-07
56 ; PRIOR APPLICATION NUMBER: 60/103328
57 ; PRIOR FILING DATE: 1998-10-07
58 ; PRIOR APPLICATION NUMBER: 60/103395
59 ; PRIOR FILING DATE: 1998-10-07
60 ; PRIOR APPLICATION NUMBER: 60/103396
61 ; PRIOR FILING DATE: 1998-10-07
62 ; PRIOR APPLICATION NUMBER: 60/103401
63 ; PRIOR FILING DATE: 1998-10-07
64 ; PRIOR APPLICATION NUMBER: 60/103449
65 ; PRIOR FILING DATE: 1998-10-06
66 ; PRIOR APPLICATION NUMBER: 60/103633
67 ; PRIOR FILING DATE: 1998-10-08
68 ; PRIOR APPLICATION NUMBER: 60/103678
69 ; PRIOR FILING DATE: 1998-10-08
70 ; PRIOR APPLICATION NUMBER: 60/103679
71 ; PRIOR FILING DATE: 1998-10-08
72 ; PRIOR APPLICATION NUMBER: 60/103711
73 ; PRIOR FILING DATE: 1998-10-08

PRIOR APPLICATION NUMBER: 60/104257
PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: 60/104987
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105002
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105104
PRIOR FILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/105169
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105266
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

Query Match 96.1%; Score 998; DB 10; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCCTTATCGCTTTCGCGTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 73
DB 1 CCGTATCGCTTTCGCGTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 60

QY 74 CGCTGACCCAGAGATGCGCCCGGAGCGAGGAAATTCCTACTGTCGGCTGCGCGCTACCG 133
DB 61 CGCTGACCCAGAGATGCGCCCGGAGCGAGGAAATTCCTACTGTCGGCTGCGCGCTACCG 120

QY 134 TGCGCCGAGCTAGCAACTTTCCTCGATCTCAAAAACTCGACTTCCAAATCAAGGAG 193
DB 121 TGCGCCGAGCTAGCAACTTTCCTCGATCTCAAAAACTCGACTTCCAAATCAAGGAG 180

QY 194 AACGAGCTTTCGCTCGGTTGGGAGCGGTCCAGAGAAATCTGCCCTATAGGGGAATGG 253
DB 181 AAGCAGCTTTCGCTCGGTTGGGAGCGGTCCAGAGAAATCTGCCCTATAGGGGAATGG 240

QY 254 TGCGCCAGCTTTCGCTCGGTTGGGAGCGGTCCAGAGAAATCTGCCCTATAGGGGAATGG 313
DB 181 AAGCAGCTTTCGCTCGGTTGGGAGCGGTCCAGAGAAATCTGCCCTATAGGGGAATGG 240

QY 254 TGCGCCAGCTTTCGCTCGGTTGGGAGCGGTCCAGAGAAATCTGCCCTATAGGGGAATGG 313
DB 181 AAGCAGCTTTCGCTCGGTTGGGAGCGGTCCAGAGAAATCTGCCCTATAGGGGAATGG 240

QY 241 TGCGCCAGCTTTCGCTCGGTTGGGAGCGGTCCAGAGAAATCTGCCCTATAGGGGAATGG 300
DB 314 CACCCGCACTTACAGACAGTGTGATTCGAGGCTCAATGCTCAGATATGACATC 373
DB 301 CACCCGCACTTACAGACAGTGTGATTCGAGGCTCAATGCTCAGATATGACATC 360

QY 374 TCCGAGAGGTTGTGTTGGCAAAAGTGAAGATGAGCATATCCCTTTGGAAATCAGTCA 433
DB 361 TCCGAGAGGTTGTGTTGGCAAAAGTGAAGATGAGCATATCCCTTTGGAAATCAGTCA 420

QY 434 TTGGAGGATGATGCTGTGTTTATTTGGCCAGTTTATTTAGCCAAATCCAACTGACTAGTGA 493
DB 421 TTGGAGGATGATGCTGTGTTTATTTGGCCAGTTTATTTAGCCAAATCCAACTGACTAGTGA 480

QY 494 AGCTTCAGATGCAATTCGAGGAAAGGAACTGAGGAAACCAATTCGGATTTTCGTG 553
DB 481 AGCTTCAGATGCAATTCGAGGAAAGGAACTGAGGAAACCAATTCGGATTTTCGTG 540

QY 554 GTGTACATCATGCTATTTGCAAAATCTTAGCTGAAGGAGGAATACGAGGCTTTTGGGAG 613
DB 541 GTGTACATCATGCTATTTGCAAAATCTTAGCTGAAGGAGGAATACGAGGCTTTTGGGAG 600

QY 614 GCTGGGTACCCATATACAAAGAGCAGCACTGTGTAATATGGGAGATTTAAACCACTTATG 673
DB 601 GCTGGGTACCCATATACAAAGAGCAGCACTGTGTAATATGGGAGATTTAAACCACTTATG 660

QY 674 ATACAGTGAACACTACTTGGTATGNAATACACCACTTGGAGCAATATCATGACTCAAG 733
DB 661 ATACAGTGAACACTACTTGGTATGNAATACACCACTTGGAGCAATATCATGACTCAAG 720

QY 734 GTTTATCAAGTTTATGTTCTGGACTGTGTAGCTTCTATTCTGGGAAACACCGCGGATGCA 793

DB 721 GTTTATCAAGTTTATGTTCTGGACTGTGTAGCTTCTATTCTGGGAACACCGCGGATGCA 780
QY 794 TCAAAAGCAGAATAAATGAATCAACACGAGATAAACAAGGAAGGGGACTTTTGTATAAAT 853
DB 781 TCAAAAGCAGAATAAATGAATCAACACGAGATAAACAAGGAAGGGGACTTTTGTATAAAT 840
QY 854 CATCGACTGACTGCTTTCGATTCAGGCTGTTCAGGTTGAAGGATTCATGAGTCTATATAAAG 913
DB 841 CATCGACTGACTGCTTTCGATTCAGGCTGTTCAGGTTGAAGGATTCATGAGTCTATATAAAG 900
QY 914 GCTTTTATACATCTTCGCTGAGAAATGACCCCTTGGTCAATGCTGCTTTCGCTTACTTATG 973
DB 901 GCTTTTATACATCTTCGCTGAGAAATGACCCCTTGGTCAATGCTGCTTTCGCTTACTTATG 960
QY 974 AAAAAATCAGAGAGATCAGTGGAGTCACTCATTTTAA 1011
DB 961 AAAAAATCAGAGAGATCAGTGGAGTCACTCATTTTAA 998

RESULT 2

US-10-015-395A-405
; Sequence 405, Application US/10015395A
; Publication No. US20040073015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C57
; CURRENT APPLICATION NUMBER: US/10/015,395A
; CURRENT FILING DATE: 2001-12-12
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 405
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-395A-405

Query Match 96.1%; Score 998; DB 12; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCCTTATCGCTTTCGCGTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 73
DB 1 CCGTATCGCTTTCGCGTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 60

QY 74 CGCTGACCCAGAGATGCGCCCGGAGCGAGGAAATTCCTACTGTCGGCTGCGCGCTACCG 133
DB 61 CGCTGACCCAGAGATGCGCCCGGAGCGAGGAAATTCCTACTGTCGGCTGCGCGCTACCG 120

QY 134 TGCGCCGAGCTAGCAACTTTCCTCGATCTCAAAAACTCGACTTCCAAATCAAGGAG 193
DB 121 TGCGCCGAGCTAGCAACTTTCCTCGATCTCAAAAACTCGACTTCCAAATCAAGGAG 180

QY 194 AACGAGCTTTCGCTCGGTTGGGAGCGGTCCAGAGAAATCTGCCCTATAGGGGAATGG 253
DB 181 AAGCAGCTTTCGCTCGGTTGGGAGCGGTCCAGAGAAATCTGCCCTATAGGGGAATGG 240

QY 254 TGCGCCAGCTTTCGCTCGGTTGGGAGCGGTCCAGAGAAATCTGCCCTATAGGGGAATGG 313

Db 241 TCGGCACAGCCCTAGGGATCAITTAAGAGGAGGCTTTCTAAGCTTTGGCAGAGGTGA 300
QY 314 CACCCGCCATTTACAGACACGTAGTGTATTCTGGAGGTGCAATGTCATATGAACATC 373
Db 301 CACCCGCCATTTACAGACACGTAGTGTATTCTGGAGGTGCAATGTCATATGAACATC 360
QY 374 TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGACATATCCCTTTGGAAATCAGTCA 433
Db 361 TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGACATATCCCTTTGGAAATCAGTCA 420
QY 434 TTGGAGGATGATGCTGCTGTTATTTGGCCAGTCTTTTAGCCAAATCCAACTGACCTAGTGA 493
Db 421 TTGGAGGATGATGCTGCTGTTATTTGGCCAGTCTTTTAGCCAAATCCAACTGACCTAGTGA 480
QY 494 AGGTTACAGTGCMAATGAAGAAAGAAAGAAATCTGGAAGAAAGAAACCAATGCGATTCGTG 553
Db 481 AGGTTACAGTGCMAATGAAGAAAGAAAGAAATCTGGAAGAAAGAAACCAATGCGATTCGTG 540
QY 554 GTGTACATCATGCAATTTGCAAAATCTTTAGCTGAAGAGGAATACGAGGGCTTTGGGCAG 613
Db 541 GTGTACATCATGCAATTTGCAAAATCTTTAGCTGAAGAGGAATACGAGGGCTTTGGGCAG 600
QY 614 GCTGGTACCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAACCACCTATG 673
Db 601 GCTGGTACCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAACCACCTATG 660
QY 674 ATACAGTGAACACTACTTGTGATTAATACACACCTTGAAGACAAATCATGACTCAG 733
Db 661 ATACAGTGAACACTACTTGTGATTAATACACACCTTGAAGACAAATCATGACTCAG 720
QY 734 GTTTATCAAGTTTATGTTCTGCACTGGTAGCTTCTATTCTGGGAACACCAAGGGGCTTTGATAAAT 793
Db 721 GTTTATCAAGTTTATGTTCTGCACTGGTAGCTTCTATTCTGGGAACACCAAGGGGCTTTGATAAAT 780
QY 794 TCAAAAGCAGAAATTAATGAATCAACACAGAGATAAACAAGGAAGGGGCTTTGATAAAT 853
Db 781 TCAAAAGCAGAAATTAATGAATCAACACAGAGATAAACAAGGAAGGGGCTTTGATAAAT 840
QY 854 CATGACTGACTGCTTGCATGAGCTCTCAAGGTGAAGATTCATGAGTCTATATAAG 913
Db 841 CATGACTGACTGCTTGCATGAGCTCTCAAGGTGAAGATTCATGAGTCTATATAAG 900
QY 914 GCTTTTACCATCTTGGCTGAGATGACCCCTTGGTCAATGCTTCTGGCTTACTTATG 973
Db 901 GCTTTTACCATCTTGGCTGAGATGACCCCTTGGTCAATGCTTCTGGCTTACTTATG 960
QY 974 AAAAAATCAGAGATGAGTGGAGTCAAGTCAATTTTAA 1011
Db 961 AAAAAATCAGAGATGAGTGGAGTCAAGTCAATTTTAA 998

RESULT 3

US-10-063-745-125

; Sequence 125, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170

; SEQ ID NO 125
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-745-125

Query Match 96.1%; Score 998; DB 13; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCGTTATCGTCTTGGCGTACTGCTGAATGTCCTGCCGAGGAGGAGGAGGCTTTTGC 73
Db 1 CCGTTATCGTCTTGGCGTACTGCTGAATGTCCTGCCGAGGAGGAGGAGGCTTTTGC 60
QY 74 CGTGACCCAGAGATGGCCCGGAGCAGCAAAATTCCTACTGTCTCGGCTGCGCGCTACCG 133
Db 61 CGTGACCCAGAGATGGCCCGGAGCAGCAAAATTCCTACTGTCTCGGCTGCGCGCTACCG 120
QY 134 TGGCCGAGCTAGCAACCTTTCCCTCGATCTCAAAAACCTCGACTCCAAATCGAAGGAG 193
Db 121 TGGCCGAGCTAGCAACCTTTCCCTCGATCTCAAAAACCTCGACTCCAAATCGAAGGAG 180
QY 194 AAGCAGCTCTTGTCTCGGTTGGGAGACGGTGCAGAGAAATCTGCCCTATAGGGGAATGG 253
Db 181 AAGCAGCTCTTGTCTCGGTTGGGAGACGGTGCAGAGAAATCTGCCCTATAGGGGAATGG 240
QY 254 TGGCAGCAGCCCTAGGGATCAITTAAGAGAAAGGCTTTCTAAAGCTTTGGCAAGGAGTGA 313
Db 241 TGGCAGCAGCCCTAGGGATCAITTAAGAGAAAGGCTTTCTAAAGCTTTGGCAAGGAGTGA 300
QY 314 CACCCGCCATTTACAGACACGTAGTGTATTCTGAGGTGCAATGTCATATGAACATC 373
Db 301 CACCCGCCATTTACAGACACGTAGTGTATTCTGAGGTGCAATGTCATATGAACATC 360
QY 374 TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAGCAATATCCCTTTGCAAAATCAGTCA 433
Db 361 TCCGAGAGGTGTGTTTGGCAAAAGTGAAGATGAGCAATATCCCTTTGCAAAATCAGTCA 420
QY 434 TTGGAGGATGATGCTGCTGTTATTTGGCCAGTCTTTTAGCCAAATCCAACTGACCTAGTGA 493
Db 421 TTGGAGGATGATGCTGCTGTTATTTGGCCAGTCTTTTAGCCAAATCCAACTGACCTAGTGA 480
QY 494 AGGTTACAGATGCAAAATGAAGAAAGAAAGAAACTTGAAGGAAGAAACCAATGCGATTCGTG 553
Db 481 AGGTTACAGATGCAAAATGAAGAAAGAAAGAAACTTGAAGGAAGAAACCAATGCGATTCGTG 540
QY 554 GTGTACATCATGCAATTTGCAAAATCTTTAGCTGAAGAGGAATACGAGGGCTTTGGGCAG 613
Db 541 GTGTACATCATGCAATTTGCAAAATCTTTAGCTGAAGAGGAATACGAGGGCTTTGGGCAG 600
QY 614 GCTGGTACCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAACCACCTATG 673
Db 601 GCTGGTACCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAACCACCTATG 660
QY 674 ATACAGTGAACACTACTTGTGATTAATACACACCTTGAAGACAAATCATGACTCAG 733
Db 661 ATACAGTGAACACTACTTGTGATTAATACACACCTTGAAGACAAATCATGACTCAG 720
QY 734 GTTTATCAAGTTTATGTTCTGCACTGGTAGCTTCTATTCTGGGAACACCAAGGGGCTTTGATAAAT 793
Db 721 GTTTATCAAGTTTATGTTCTGCACTGGTAGCTTCTATTCTGGGAACACCAAGGGGCTTTGATAAAT 780
QY 794 TCAAAAGCAGAAATTAATGAATCAACACAGAGATAAACAAGGAAGGGGCTTTGATAAAT 853
Db 781 TCAAAAGCAGAAATTAATGAATCAACACAGAGATAAACAAGGAAGGGGCTTTGATAAAT 840
QY 854 CATGACTGACTGCTTGCATGAGCTCTCAAGGTGAAGATTCATGAGTCTATATAAG 913
Db 841 CATGACTGACTGCTTGCATGAGCTCTCAAGGTGAAGATTCATGAGTCTATATAAG 900
QY 914 GCTTTTACCATCTTGGCTGAGATGACCCCTTGGTCAATGCTTCTGGCTTACTTATG 973
Db 901 GCTTTTACCATCTTGGCTGAGATGACCCCTTGGTCAATGCTTCTGGCTTACTTATG 960

QY	974	AAAAATCAGAGATGAGTGGAGTCAGTCCATTATAA	1011
Db	961	AAAAATCAGAGATGAGTGGAGTCAGTCCATTATAA	998
RESULT 4			
US-10-063-512-125			
; Sequence 125, Application US/10063512			
; Publication No. US20030018172A1			
; GENERAL INFORMATION:			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, Christopher J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Wood, William I.			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; FILE REFERENCE: P3230R1C1			
; CURRENT APPLICATION NUMBER: US/10/063, 512			
; Prior Application removed - See File Wrapper or Palm			
; NUMBER OF SEQ ID NOS: 170			
; SEQ ID NO 125			
; LENGTH: 998			
; TYPE: DNA			
; ORGANISM: Homo Sapien			
US-10-063-512-125			
Query Match			
Best Local Similarity 96.1%; Score 998; DB 13; Length 998;			
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	14	CCGTTATCGTCTTGGCGTACTGCTGAATGTCCTCCGGAGGAGGAGGAGGCTTTTGC	73
Db	1	CCGTTATCGTCTTGGCGTACTGCTGAATGTCCTCCGGAGGAGGAGGAGGCTTTTGC	60
QY	74	CGTGACCCAGAGATGGCCCGAGCGAGCAAAATTCCTACTGTCCGGCTGCGGGTACCG	133
Db	61	CGTGACCCAGAGATGGCCCGAGCGAGCAAAATTCCTACTGTCCGGCTGCGGGTACCG	120
QY	134	TGCGCCAGCTAGCAACCTTCCCTCGATCTCAAAAATCGACTCCAAATCCAGGAG	193
Db	121	TGCGCCAGCTAGCAACCTTCCCTCGATCTCAAAAATCGACTCCAAATCCAGGAG	180
QY	194	AAGCAGCTCTTGTCTGGGAGACGGTGCAGAGAAATCTGCCCTATAGGGGAATGG	253
Db	181	AAGCAGCTCTTGTCTGGGAGACGGTGCAGAGAAATCTGCCCTATAGGGGAATGG	240
QY	254	TGCGCACAGCCCTAGGGATCATTAAGAGAGAGGCTTTCTAAAGCTTTGGCAAGAGTGA	313
Db	241	TGCGCACAGCCCTAGGGATCATTAAGAGAGAGGCTTTCTAAAGCTTTGGCAAGAGTGA	300
QY	314	CACCCGCCATTTACACACAGTGTATCTCGAGGTGCAATGGTCCACATATGAACATC	373
Db	301	CACCCGCCATTTACACACAGTGTATCTCGAGGTGCAATGGTCCACATATGAACATC	360
QY	374	TCCGAGAGGTGTGTTTGGCAAAATGAAGATCAGCATTAATCCCTTTTGGAAATCAGTCA	433
Db	361	TCCGAGAGGTGTGTTTGGCAAAATGAAGATCAGCATTAATCCCTTTTGGAAATCAGTCA	420
QY	434	TTGGAGGATGATGGCTGTGTTTATTTGGCCAGTTTTTACCAATCCAACTGACCTAGTGA	493
Db	421	TTGGAGGATGATGGCTGTGTTTATTTGGCCAGTTTTTACCAATCCAACTGACCTAGTGA	480
QY	494	AGTTTCAGATGCAATGGAGGAAAAAGAAATCGAAGGAAAAACCATTCGCAATTCGTCG	553
Db	481	AGTTTCAGATGCAATGGAGGAAAAAGAAATCGAAGGAAAAACCATTCGCAATTCGTCG	540

RESULT 5			
US-10-063-513-125			
; Sequence 125, Application US/10063513			
; Publication No. US20030018172A1			
; GENERAL INFORMATION:			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, Christopher J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Wood, William I.			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; FILE REFERENCE: P3230R1C1			
; CURRENT APPLICATION NUMBER: US/10/063, 513			
; Prior Application removed - See File Wrapper or Palm			
; NUMBER OF SEQ ID NOS: 170			
; SEQ ID NO 125			
; LENGTH: 998			
; TYPE: DNA			
; ORGANISM: Homo Sapien			
US-10-063-513-125			
Query Match			
Best Local Similarity 96.1%; Score 998; DB 13; Length 998;			
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	14	CCGTTATCGTCTTGGCGTACTGCTGAATGTCCTCCGGAGGAGGAGGAGGCTTTTGC	73
Db	1	CCGTTATCGTCTTGGCGTACTGCTGAATGTCCTCCGGAGGAGGAGGAGGCTTTTGC	60
QY	74	CGTGACCCAGAGATGGCCCGAGCGAGCAAAATTCCTACTGTCCGGCTGCGGGTACCG	133
Db	61	CGTGACCCAGAGATGGCCCGAGCGAGCAAAATTCCTACTGTCCGGCTGCGGGTACCG	120
QY	134	TGCGCCAGCTAGCAACCTTCCCTCGATCTCAAAAATCGACTCCAAATCCAGGAG	193

```

Db 121 TGGCCGAGCTAGCAACCTTCCCTGGATCTCACAAAACCTCGACTCAATGCAAGAG 180
Qy 134 AAGAGCTCTTCTCGTGGGAGACGGTGCAGAGAAATCTGCCCTTATAGGGAATGG 253
Db 181 AAGAGCTCTTCTCGTGGGAGACGGTGCAGAGAAATCTGCCCTTATAGGGAATGG 240
Qy 254 TGGCCGAGCTAGCAACCTTCCCTGGATCTCACAAAACCTCGACTCAATGCAAGAG 313
Db 241 TGGCCGAGCTAGCAACCTTCCCTGGATCTCACAAAACCTCGACTCAATGCAAGAG 300
Qy 314 CACCGCCATTTACAGACACCTAGTGTATCTGAGGTGCAATGCTCAATCAACATC 373
Db 301 CACCGCCATTTACAGACACCTAGTGTATCTGAGGTGCAATGCTCAATCAACATC 360
Qy 374 TCCGAGAGGTGTGTTGGGAAAGTGAAGATGAGCAATATCCCTTTGGAAATCAGTCA 433
Db 361 TCCGAGAGGTGTGTTGGGAAAGTGAAGATGAGCAATATCCCTTTGGAAATCAGTCA 420
Qy 434 TGGAGGATGATGGCTGGTGTATTTGGCCAGTATTTAGCCAACTCCAACTGACCTAGTGA 493
Db 421 TGGAGGATGATGGCTGGTGTATTTGGCCAGTATTTAGCCAACTCCAACTGACCTAGTGA 480
Qy 494 AGGTTACAGTCAATGCAACCTAGTGTATTTGGCCAGTATTTAGCCAACTCCAACTGACCTAGTGA 553
Db 481 AGGTTACAGTCAATGCAACCTAGTGTATTTGGCCAGTATTTAGCCAACTCCAACTGACCTAGTGA 540
Qy 554 GTGTACATCATGCAATTTGCAAAATCTTAGCTGAAGAGAAATGAGAGGGCTTTGGGCGAG 613
Db 541 GTGTACATCATGCAATTTGCAAAATCTTAGCTGAAGAGAAATGAGAGGGCTTTGGGCGAG 600
Qy 614 GCTGGTACCAATATACAAAGACGACCTGTGTGAATATGGGAGATTTAAACCACTTATG 673
Db 601 GCTGGTACCAATATACAAAGACGACCTGTGTGAATATGGGAGATTTAAACCACTTATG 660
Qy 674 ATACAGTGAACATCTATGTTGTAATACCACTTTGAGGACAAATATCATGACTCAG 733
Db 661 ATACAGTGAACATCTATGTTGTAATACCACTTTGAGGACAAATATCATGACTCAG 720
Qy 734 GTTTATCAAGTTTATGTTCTGACTGTGATTTAGCCAACTCCAACTGACCTTATG 780
Db 721 GTTTATCAAGTTTATGTTCTGACTGTGATTTAGCCAACTCCAACTGACCTTATG 770
Qy 794 TCAAAAGCAGAAATGAATCAACACGAGATAAAACAGGAGGAGGACTTTTGTATAAAT 853
Db 781 TCAAAAGCAGAAATGAATCAACACGAGATAAAACAGGAGGAGGACTTTTGTATAAAT 840
Qy 854 CATGACTGACTGCTTGAATTCAGCTGTTCAAGGTGAAGATTCATGAGTCTATATAAG 913
Db 841 CATGACTGACTGCTTGAATTCAGCTGTTCAAGGTGAAGATTCATGAGTCTATATAAG 900
Qy 914 GCTTTTACCACCTTGGCTGAGATGACCTTGGTCAATGAGTGTCTGGCTTACTTATG 973
Db 901 GCTTTTACCACCTTGGCTGAGATGACCTTGGTCAATGAGTGTCTGGCTTACTTATG 960
Qy 974 AAAAAATCAGAGATGAGTGGAGTCAATCCATTTTAA 1011
Db 961 AAAAAATCAGAGATGAGTGGAGTCAATCCATTTTAA 998

```

RESULT 6

US-10-063-569-125
; Sequence 125, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 125
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-063-569-125

Query Match 96.1%; Score 998; DB 13; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 14 CCCTTATCGTCTTGGCGTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 73
Db 1 CCCTTATCGTCTTGGCGTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 60
Qy 74 CGCTGACCCAGAGATGCGCCCGAGCGAGCAAAATTCCTACTGTCGCGCTGCGCGCTACCG 133
Db 61 CGCTGACCCAGAGATGCGCCCGAGCGAGCAAAATTCCTACTGTCGCGCTGCGCGCTACCG 120
Qy 134 TGGCCGAGCTAGCAACCTTTCCTCCGATCTCAAAAACTCGACTCCAAATGCAAGGAG 193
Db 121 TGGCCGAGCTAGCAACCTTTCCTCCGATCTCAAAAACTCGACTCCAAATGCAAGGAG 180
Qy 194 AAGCAGCTCTTCTCGTGGGAGACGGTGCAGAGAAATGCGCCCTATAGGGAATGG 253
Db 181 AAGCAGCTCTTCTCGTGGGAGACGGTGCAGAGAAATGCGCCCTATAGGGAATGG 240
Qy 254 TGGCCAGCCCTTAGGGATCATTTGAAGAGAAAGGCTTTTAAAGCTTTTGGCAAGGAGTGA 313
Db 241 TGGCCAGCCCTTAGGGATCATTTGAAGAGAAAGGCTTTTAAAGCTTTTGGCAAGGAGTGA 300
Qy 314 CACCGCCATTTACAGACACCTAGTGTATTTCTGAGGTGCAATGCTCAATATGAACATC 373
Db 301 CACCGCCATTTACAGACACCTAGTGTATTTCTGAGGTGCAATGCTCAATATGAACATC 360
Qy 374 TCCGAGAGGTGTGTTGGCAAAAGTGAAGATGAGCAATATCCCTTTTGGAAATCAGTCA 433
Db 361 TCCGAGAGGTGTGTTGGCAAAAGTGAAGATGAGCAATATCCCTTTTGGAAATCAGTCA 420
Qy 434 TGGAGGAGATGAGTGGTGTATTTGGCCAGTATTTAGCCAACTCCAACTGACCTAGTGA 493
Db 421 TGGAGGAGATGAGTGGTGTATTTGGCCAGTATTTAGCCAACTCCAACTGACCTAGTGA 480
Qy 494 AGGTTACAGTCAATGCAACCTAGGAGAAAGAACTCGAAGGAAACCATTTGCCATTCGTG 553
Db 481 AGGTTACAGTCAATGCAACCTAGGAGAAAGAAAGAACTCGAAGGAAACCATTTGCCATTCGTG 540
Qy 554 GTGTACATCATGCAATTTGCAAAATCTTAGCTGAAAGAGGAAATAGAGGGCTTTTGGGCGAG 613
Db 541 GTGTACATCATGCAATTTGCAAAATCTTAGCTGAAAGAGGAAATAGAGGGCTTTTGGGCGAG 600
Qy 614 GCTGGGTACCCAAATATACAAAGAGGAGCACTGTGTGAATATGGGAGATTTAAACCACTTATG 673
Db 601 GCTGGGTACCCAAATATACAAAGAGGAGCACTGTGTGAATATGGGAGATTTAAACCACTTATG 660
Qy 674 ATACAGTGAACATCTATGTTGTAATACCACTTTGAGGACAAATATCATGACTCAG 733
Db 661 ATACAGTGAACATCTATGTTGTAATACCACTTTGAGGACAAATATCATGACTCAG 720
Qy 734 GTTTATCAAGTTTATGTTCTGACTGTGATTTAGCCAACTCCAACTGACCTTATG 780
Db 721 GTTTATCAAGTTTATGTTCTGACTGTGATTTAGCCAACTCCAACTGACCTTATG 770
Qy 794 TCAAAAGCAGAAATGAATCAACACGAGATAAAACAGGAGGAGGACTTTTGTATAAAT 853
Db 781 TCAAAAGCAGAAATGAATCAACACGAGATAAAACAGGAGGAGGACTTTTGTATAAAT 840

```


	PRIOR APPLICATION NUMBER:	60/098803
	PRIOR FILING DATE:	1998-09-02
	PRIOR APPLICATION NUMBER:	60/098821
	PRIOR FILING DATE:	1998-09-02
	PRIOR APPLICATION NUMBER:	60/098843
	PRIOR FILING DATE:	1998-09-02
	PRIOR APPLICATION NUMBER:	60/099536
	PRIOR FILING DATE:	1998-09-09
	PRIOR APPLICATION NUMBER:	60/099596
	PRIOR FILING DATE:	1998-09-09
	PRIOR APPLICATION NUMBER:	60/099598
	PRIOR FILING DATE:	1998-09-09
	PRIOR APPLICATION NUMBER:	60/099602
	PRIOR FILING DATE:	1998-09-09
	PRIOR APPLICATION NUMBER:	60/099642
	PRIOR FILING DATE:	1998-09-09
	PRIOR APPLICATION NUMBER:	60/099741
	PRIOR FILING DATE:	1998-09-10
	PRIOR APPLICATION NUMBER:	60/099754
	PRIOR FILING DATE:	1998-09-10
	PRIOR APPLICATION NUMBER:	60/099763
	PRIOR FILING DATE:	1998-09-10
	PRIOR APPLICATION NUMBER:	60/099792
	PRIOR FILING DATE:	1998-09-10
	PRIOR APPLICATION NUMBER:	60/099808
	PRIOR FILING DATE:	1998-09-10
	PRIOR APPLICATION NUMBER:	60/099812
	PRIOR FILING DATE:	1998-09-10
	PRIOR APPLICATION NUMBER:	60/099815
	PRIOR FILING DATE:	1998-09-10
	PRIOR APPLICATION NUMBER:	60/099816
	PRIOR FILING DATE:	1998-09-10
	PRIOR APPLICATION NUMBER:	60/100385
	PRIOR FILING DATE:	1998-09-15
	PRIOR APPLICATION NUMBER:	60/100388
	PRIOR FILING DATE:	1998-09-15
	PRIOR APPLICATION NUMBER:	60/100390
	PRIOR FILING DATE:	1998-09-15
	PRIOR APPLICATION NUMBER:	60/100584
	PRIOR FILING DATE:	1998-09-16
	PRIOR APPLICATION NUMBER:	60/100627
	PRIOR FILING DATE:	1998-09-16
	PRIOR APPLICATION NUMBER:	60/100661
	PRIOR FILING DATE:	1998-09-16
	PRIOR APPLICATION NUMBER:	60/100662
	PRIOR FILING DATE:	1998-09-16
	PRIOR APPLICATION NUMBER:	60/100664
	PRIOR FILING DATE:	1998-09-16
	PRIOR APPLICATION NUMBER:	60/100683
	PRIOR FILING DATE:	1998-09-17
	PRIOR APPLICATION NUMBER:	60/100684
	PRIOR FILING DATE:	1998-09-17
	PRIOR APPLICATION NUMBER:	60/100710
	PRIOR FILING DATE:	1998-09-17
	PRIOR APPLICATION NUMBER:	60/100711
	PRIOR FILING DATE:	1998-09-17
	PRIOR APPLICATION NUMBER:	60/100848
	PRIOR FILING DATE:	1998-09-18
	PRIOR APPLICATION NUMBER:	60/100849
	PRIOR FILING DATE:	1998-09-18
	PRIOR APPLICATION NUMBER:	60/100919
	PRIOR FILING DATE:	1998-09-17
	PRIOR APPLICATION NUMBER:	60/100930
	PRIOR FILING DATE:	1998-09-17
	PRIOR APPLICATION NUMBER:	60/101014
	PRIOR FILING DATE:	1998-09-18
	PRIOR APPLICATION NUMBER:	60/101068
	PRIOR FILING DATE:	1998-09-18
	PRIOR APPLICATION NUMBER:	60/101071
	PRIOR FILING DATE:	1998-09-18
	PRIOR APPLICATION NUMBER:	60/101279
	PRIOR FILING DATE:	1998-09-22
	PRIOR APPLICATION NUMBER:	60/101471

```

; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match          96.1%; Score 998; DB 13; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCGTTATCGTTTGGCGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 73
DB 1 CCGTTATCGTTTGGCGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 60

QY 74 CGCTGACCCAGAGATGGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 133
DB 61 CGCTGACCCAGAGATGGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120

QY 134 TGCGCCGAGTAGCAACTTTCCTCCCTGGATCTCAAAAAAAGTCCGACTCCAAATGCAAGGAG 193
DB 121 TGCGCCGAGTAGCAACTTTCCTCCCTGGATCTCAAAAAAAGTCCGACTCCAAATGCAAGGAG 180

QY 194 AAGCAGCTCTTGTCTGGTGGGAGACGGTGCAGAGAGAAATCTGCCCCCTATAGGGGAGTGG 253
DB 181 AAGCAGCTCTTGTCTGGTGGGAGACGGTGCAGAGAGAAATCTGCCCCCTATAGGGGAGTGG 240

QY 254 TGCGCACGCCCTAGGAGTCAATGAGAGGAGGCTTCTTAAGCTTTGGCAGGAGTGA 313
DB 241 TGCGCACGCCCTAGGAGTCAATGAGAGGAGGCTTCTTAAGCTTTGGCAGGAGTGA 300

QY 314 CACCCGCCATTTACAGACACGTAAGTCTATCTGGAGTGAATGCTCAATATGAACATC 373
DB 301 CACCCGCCATTTACAGACACGTAAGTCTATCTGGAGTGAATGCTCAATATGAACATC 360

QY 374 TCCGAGAGGTGTGTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAATCAGTCA 433
DB 361 TCCGAGAGGTGTGTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAATCAGTCA 420

QY 434 TTGGAGGGATGATGGCTGTGTTTATTTGGCCAGTTTTTAGCCATCCAACTGACCTAGTGA 493
DB 421 TTGGAGGGATGATGGCTGTGTTTATTTGGCCAGTTTTTAGCCATCCAACTGACCTAGTGA 480

QY 494 AGGTTTCAGATGCAAAATGGAAGGAAAAAGAAATCGGAAGGAAAAACATTTGCCATTTTCGTG 553
DB 481 AGGTTTCAGATGCAAAATGGAAGGAAAAAGAAATCGGAAGGAAAAACATTTGCCATTTTCGTG 540

QY 554 GTGTACATCATGCTTTGCAAAATCTTAGCTGAAGAGGAGAAATACGAGGCTTTTGGGAG 613
DB 541 GTGTACATCATGCTTTGCAAAATCTTAGCTGAAGAGGAGAAATACGAGGCTTTTGGGAG 600

QY 614 GCTGGGTACCCATATACAAAGAGCAGCACTGTGTAATATGGAGATTTAAACCACCTATG 673
DB 601 GCTGGGTACCCATATACAAAGAGCAGCACTGTGTAATATGGAGATTTAAACCACCTATG 660

674 ATACAGTGAACACTACTTGGTATTGAATACACCACTTGAGGACAATATATCATGACTCACG 733
661 ATACAGTGAACACTACTTGGTATTGAATACACCACTTGAGGACAATATATCATGACTCACG 720
734 GTTTATCAAGTTTATGTTCTGGACTGTAGCTTCTATTCTGGGAAACACCGCGGATGCA 793
721 GTTTATCAAGTTTATGTTCTGGACTGTAGCTTCTATTCTGGGAAACACCGCGGATGCA 780
794 TCAAAAGCAGAATAATGAATCAACACGAGATATAACAGGAAGGGGACTTTTGTATATAAT 853
781 TCAAAAGCAGAATAATGAATCAACACGAGATATAACAGGAAGGGGACTTTTGTATATAAT 840
854 CATCGACTGACTGCTTGTGATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAG 913
841 CATCGACTGACTGCTTGTGATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAG 900
914 GCTTTTACCATCTTGGCTTGAGNATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 973
901 GCTTTTACCATCTTGGCTTGAGNATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 960
974 AAAAAATCAGAGAGATGAGTGGAGTCAGTCCCATTTTAA 1011
961 AAAAAATCAGAGAGATGAGTGGAGTCAGTCCCATTTTAA 998

RESULT 9
US-10-013-907A-405
; Sequence 405, Application US/10013907A
; Publication No. US20030064925A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Epton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC34
; CURRENT APPLICATION NUMBER: US/10/013,907A
; CURRENT FILING DATE: 2001-12-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 405
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-013-907A-405

Query Match          96.1%; Score 998; DB 13; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCGTTATCGTTTGGCGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 73
DB 1 CCGTTATCGTTTGGCGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 60

QY 74 CGCTGACCCAGAGATGGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 133
DB 61 CGCTGACCCAGAGATGGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120

QY 134 TGCGCCGAGTAGCAACTTTCCTCCCTGGATCTCAAAAAAAGTCCGACTCCAAATGCAAGGAG 193
DB 121 TGCGCCGAGTAGCAACTTTCCTCCCTGGATCTCAAAAAAAGTCCGACTCCAAATGCAAGGAG 180

QY 194 AAGCAGCTCTTGTCTGGTGGGAGACGGTGCAGAGAGAAATCTGCCCCCTATAGGGGAGTGG 253
DB 181 AAGCAGCTCTTGTCTGGTGGGAGACGGTGCAGAGAGAAATCTGCCCCCTATAGGGGAGTGG 240

QY 254 TGCGCACGCCCTAGGAGTCAATGAGAGGAGGCTTCTTAAGCTTTGGCAGGAGTGA 313
DB 241 TGCGCACGCCCTAGGAGTCAATGAGAGGAGGCTTCTTAAGCTTTGGCAGGAGTGA 300

QY 314 CACCCGCCATTTACAGACACGTAAGTCTATCTGGAGTGAATGCTCAATATGAACATC 373
DB 301 CACCCGCCATTTACAGACACGTAAGTCTATCTGGAGTGAATGCTCAATATGAACATC 360

QY 374 TCCGAGAGGTGTGTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAATCAGTCA 433
DB 361 TCCGAGAGGTGTGTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAATCAGTCA 420

QY 434 TTGGAGGGATGATGGCTGTGTTTATTTGGCCAGTTTTTAGCCATCCAACTGACCTAGTGA 493
DB 421 TTGGAGGGATGATGGCTGTGTTTATTTGGCCAGTTTTTAGCCATCCAACTGACCTAGTGA 480

QY 494 AGGTTTCAGATGCAAAATGGAAGGAAAAAGAAATCGGAAGGAAAAACATTTGCCATTTTCGTG 553
DB 481 AGGTTTCAGATGCAAAATGGAAGGAAAAAGAAATCGGAAGGAAAAACATTTGCCATTTTCGTG 540

QY 554 GTGTACATCATGCTTTGCAAAATCTTAGCTGAAGAGGAGAAATACGAGGCTTTTGGGAG 613
DB 541 GTGTACATCATGCTTTGCAAAATCTTAGCTGAAGAGGAGAAATACGAGGCTTTTGGGAG 600

QY 614 GCTGGGTACCCATATACAAAGAGCAGCACTGTGTAATATGGAGATTTAAACCACCTATG 673
DB 601 GCTGGGTACCCATATACAAAGAGCAGCACTGTGTAATATGGAGATTTAAACCACCTATG 660
```

```

QY 194 AAGCAGCTCTTGCTCGTGGGAGACGGTCAAGAGAACTCTGCCCTATAGGGAATGG 253
Db 191 AAGCAGCTCTTGCTCGTGGGAGACGGTCAAGAGAACTCTGCCCTATAGGGAATGG 240
QY 254 TGGCAGCAGCCCTAGGGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA 313
Db 241 TGGCAGCAGCCCTAGGGATCATTTGAAGAGGAGGCTTTCTAAAGCTTTGGCAAGGAGTGA 300
QY 314 CACCGCCATTTACAGACACAGTGTATTTCTGAGGTGCAATGGTGCATATGAACATC 373
Db 301 CACCGCCATTTACAGACACAGTGTATTTCTGAGGTGCAATGGTGCATATGAACATC 360
QY 374 TCCGAGAGGTGTGTGTGGCAAAAGTGAAGATGAGCATTTATCCCTTTGGAAATCAGTCA 433
Db 361 TCCGAGAGGTGTGTGTGGCAAAAGTGAAGATGAGCATTTATCCCTTTGGAAATCAGTCA 420
QY 434 TTGGAGGATGATGGCTGGTGTATTTGGCCAGTTTATAGCCAAATCCAACTGACCTAGTGA 493
Db 421 TTGGAGGATGATGGCTGGTGTATTTGGCCAGTTTATAGCCAAATCCAACTGACCTAGTGA 480
QY 494 AGGTTACAGATCAATGCAAGGAAAGAAAGTGAAGTGAAGGAAATCCAACTGACCTAGTGA 553
Db 481 AGGTTACAGATCAATGCAAGGAAAGAAAGTGAAGTGAAGGAAATCCAACTGACCTAGTGA 540
QY 554 GTGTACATCATGATGATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 613
Db 541 GTGTACATCATGATGATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
QY 614 GCTGGGTACCCAAATATCAAGAGCAGCAGTGTGTAATATGGGAGATTTAAACCACTTATG 673
Db 601 GCTGGGTACCCAAATATCAAGAGCAGCAGTGTGTAATATGGGAGATTTAAACCACTTATG 660
QY 674 ATACAGTGAACACTACTTGTGTAATATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 733
Db 661 ATACAGTGAACACTACTTGTGTAATATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 734 GTTTATCAAGTTTATGTTCTGGACTGGTGTCTTATTTGGGAAACACAGCCGATGTC 793
Db 721 GTTTATCAAGTTTATGTTCTGGACTGGTGTCTTATTTGGGAAACACAGCCGATGTC 780
QY 794 TCRAAGCAGATTAATGAATCAACACAGATTAATGAAGGAGGAGGAGGAGGAGGAGGAGGAG 853
Db 781 TCRAAGCAGATTAATGAATCAACACAGATTAATGAAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 854 CATGCTGACTGCTGCTGATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAG 913
Db 841 CATGCTGACTGCTGCTGATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAG 900
QY 914 GCTTTTACCATCTTGGCTGAGATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 973
Db 901 GCTTTTACCATCTTGGCTGAGATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 960
QY 974 AAAAAATCAGAGATGAGTGGAGTCACTCAGTCCATTTAA 1011
Db 961 AAAAAATCAGAGATGAGTGGAGTCACTCAGTCCATTTAA 998

```

RESULT 10

```

US-10-015-499A-405
; Sequence 405 Application US/10015499A
; Publication No. US20030065142A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.

```

```

; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C42
; CURRENT APPLICATION NUMBER: US/10/015,499A
; CURRENT FILING DATE: 2001-12-11
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 405
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-499A-405

Query Match 96.1%; Score 998; DB 13; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCCTTATCGTCTTGGCGTACTGCTGAATGTCCTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAG 73
Db 1 CCCTTATCGTCTTGGCGTACTGCTGAATGTCCTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
QY 74 CGCTGACCCAGAGATGCGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 133
Db 61 CGCTGACCCAGAGATGCGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
QY 134 TGCCCGAGCTAGCAACCTTTCCCTCGTGTCTCACAAAAAATCGACCTCCAAATGCAAGGAG 193
Db 121 TGCCCGAGCTAGCAACCTTTCCCTCGTGTCTCACAAAAAATCGACCTCCAAATGCAAGGAG 180
QY 194 AAGCAGCTCTTGTGCTGGTGGGAGACGGTGAAGAGAAATCTGCCCTATAGGGAATGG 253
Db 181 AAGCAGCTCTTGTGCTGGTGGGAGACGGTGAAGAGAAATCTGCCCTATAGGGAATGG 240
QY 254 TGGCAGCAGCCCTAGGGATCATTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 313
Db 241 TGGCAGCAGCCCTAGGGATCATTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
QY 314 CACCGCCATTTACAGACACGATGATGTAATTTGGAGGTGCAATGTCATATGAACATC 373
Db 301 CACCGCCATTTACAGACACGATGATGTAATTTGGAGGTGCAATGTCATATGAACATC 360
QY 374 TCCGAGAGGTGCTGTTGGCAAAAGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 433
Db 361 TCCGAGAGGTGCTGTTGGCAAAAGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 434 TTGGAGGATGATGGCTGGTGTATTTGGCCAGTTTATAGCCAAATCCAACTGACCTAGTGA 493
Db 421 TTGGAGGATGATGGCTGGTGTATTTGGCCAGTTTATAGCCAAATCCAACTGACCTAGTGA 480
QY 494 AGGTTACAGATCAATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 553
Db 481 AGGTTACAGATCAATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 554 GTGTACATCATGCTTTCGCAAAATCTTAGCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 613
Db 541 GTGTACATCATGCTTTCGCAAAATCTTAGCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
QY 614 GCTGGGTACCCAAATATCAAGAGCAGCAGTGTGTAATATGGGAGATTTAAACCACTTATG 673
Db 601 GCTGGGTACCCAAATATCAAGAGCAGCAGTGTGTAATATGGGAGATTTAAACCACTTATG 660
QY 674 ATACAGTGAACACTACTTGTGTAATATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 733
Db 661 ATACAGTGAACACTACTTGTGTAATATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 734 GTTTATCAAGTTTATGTTCTGGACTGGTGTCTTATTTGGGAAACACAGCCGATGTC 793
Db 721 GTTTATCAAGTTTATGTTCTGGACTGGTGTCTTATTTGGGAAACACAGCCGATGTC 780
QY 794 TCRAAGCAGATTAATGAATCAACAGAGATTAATGAAGGAGGAGGAGGAGGAGGAGGAGGAG 853

```

```
Db 781 TCAAAAGCAGATAAATGAATCAACACGAGATATAAAGGAGGAGCTTTTGTATAAAT 840
QY 854 CATCGAGTACTGCTTCAATCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAG 913
Db 841 CATCGAGTACTGCTTCAATCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAG 900
QY 914 GCTTTTACCACCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTCGCTTACTTATG 973
Db 901 GCTTTTACCACCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTCGCTTACTTATG 960
QY 974 AAAAAATCAGAGATGAGTGGAGTCAATCAATTTAA 1011
Db 961 AAAAAATCAGAGATGAGTGGAGTCAATCAATTTAA 998

RESULT 11
US-10-063-555-125
; Sequence 125, Application US/10063555
; Publication No. US20030065143A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,555
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 125
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-555-125
```

```
Query Match 96.1%; Score 998; DB 13; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCCTTATCGTCTTGGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 73
Db 1 CCCTTATCGTCTTGGCTACTGCTGAATGTCCTCCGAGGAGGAGGAGGCTTTTGC 60
QY 74 CGCTGACCCAGAGATGCCCGGAGCGAGCAAAATTCCTACTGTCGGCTGCGGCTACCG 133
Db 61 CGCTGACCCAGAGATGCCCGGAGCGAGCAAAATTCCTACTGTCGGCTGCGGCTACCG 120
QY 134 TGCCCGAGCTAGCAACTTTCCTCCCTGGATCTCAAAAACTCGACTCCAAATGCAAGGAG 193
Db 121 TGCCCGAGCTAGCAACTTTCCTCCCTGGATCTCAAAAACTCGACTCCAAATGCAAGGAG 180
QY 194 AGCAGCTTCTGCTGGTGGGAGACGGTGCAGAGAAATTCGCCCTATAGGGGAATGG 253
Db 181 AGCAGCTTCTGCTGGTGGGAGACGGTGCAGAGAAATTCGCCCTATAGGGGAATGG 240
QY 254 TGCGCACGCCCTAGGATCAATGAGAGGAGGCTTCTAAAGCTTTGGCAAGGATGA 313
Db 241 TGCGCACGCCCTAGGATCAATGAGAGGAGGCTTCTAAAGCTTTGGCAAGGATGA 300
QY 314 CACCCGCCATTTACAGACAGTGTATTTCTGGAGTGAATGGTCAATATGAACATC 373
Db 301 CACCCGCCATTTACAGACAGTGTATTTCTGGAGTGAATGGTCAATATGAACATC 360
QY 374 TCCGAGAGGTTGTGTTGGCAAAAGTCAAGATGAGCATTTATCCCTTTTGGAAATCAGTCA 433
```

```
Db 361 TCCGAGAGGTTGTGTTGGCAAAAGTGAAGATGAGCATTTATCCCTTTTGGAAATCAGTCA 420
QY 434 TTGGAGGATGATGGCTGGTGTGTTATTGGCCAGTGTGTTTAGCCAAATCCAACTAGTGA 493
Db 421 TTGGAGGATGATGGCTGGTGTGTTATTGGCCAGTGTGTTTAGCCAAATCCAACTAGTGA 480
QY 494 AGGTTTCAAGTGCATAATGGAAAGGAAAGGAACTTGAAGGAAACCAATTCGATTTCTGTG 553
Db 481 AGGTTTCAAGTGCATAATGGAAAGGAAAGGAACTTGAAGGAAACCAATTCGATTTCTGTG 540
QY 554 GTGTATCATGCTATTTGCAAAATCTTAGCTGAAGGAGAAATACGAGGGCTTTGGGCGAG 613
Db 541 GTGTATCATGCTATTTGCAAAATCTTAGCTGAAGGAGAAATACGAGGGCTTTGGGCGAG 600
QY 614 GCTGGGTACCCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 673
Db 601 GCTGGGTACCCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTAAACCACTTATG 660
QY 674 ATACAGTGAACACTTCTGGTATTGAATACACACTTTGAGGACAATATCATGACTCACG 733
Db 661 ATACAGTGAACACTTCTGGTATTGAATACACACTTTGAGGACAATATCATGACTCACG 720
QY 734 GTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGACACCGCGATGTC 793
Db 721 GTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGACACCGCGATGTC 780
QY 794 TCAAAAGCAGATAAATGAATCAACACGAGATATAAAGGAAAGGGGACTTTTGTATAAAT 853
Db 781 TCAAAAGCAGATAAATGAATCAACACGAGATATAAAGGAAAGGGGACTTTTGTATAAAT 840
QY 854 CATCGACTGACTGCTTGTGATTCAAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAG 913
Db 841 CATCGACTGACTGCTTGTGATTCAAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAG 900
QY 914 GCTTTTACCACCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTCGCTTACTTATG 973
Db 901 GCTTTTACCACCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTCGCTTACTTATG 960
QY 974 AAAAAATCAGAGATGAGTGGAGTCAATCAATTTAA 1011
Db 961 AAAAAATCAGAGATGAGTGGAGTCAATCAATTTAA 998
```

RESULT 12

```
US-10-063-563-125
; Sequence 125, Application US/10063563
; Publication No. US20030060602A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,563
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 125
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-563-125
```

```
Query Match 96.1%; Score 998; DB 13; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```
Db 661 ATACAGTGAACACTACTTGGTATTGAATACCACTTGGAGCAATATCATGACTCACG 720
Qy 734 GTTTATCAAGCTTTATGTTCTGGACTGTAGTCTTCTATTCTGGGAACACACCGCGATGTCA 793
Db 721 GTTTATCAAGCTTTATGTTCTGGACTGTAGTCTTCTATTCTGGGAACACACCGCGATGTCA 780
Qy 794 TCAAAAGCAGAAATTAATCAATCAACACGAGATAAACAAAGGAAGGGGACTTTTGTATAAAT 853
Db 781 TCAAAAGCAGAAATTAATCAATCAACACGAGATAAACAAAGGAAGGGGACTTTTGTATAAAT 840
Qy 854 CATGACTGACTGCTTGTATTCAGCTGTTCAGGCTGTTCAGGTAAGGATTCATGAGTCTATATAAG 913
Db 841 CATGCACTGACTGCTTGTATTCAGGCTGTTCAGGCTGTTCAGGTAAGGATTCATGAGTCTATATAAG 900
Qy 914 GCTTTTACCACCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 973
Db 901 GCTTTTACCACCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 960
Qy 974 AAAAAATCAGAGAGATGAGTGGAGTCAGTCCATTTTAA 1011
Db 961 AAAAAATCAGAGAGATGAGTGGAGTCAGTCCATTTTAA 998
```

RESULT 14

```
US-10-063-553-125
; Sequence 125, Application US/10063553
; Publication No. US20030045684A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,553
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 125
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-553-125
```

```
Query Match 96.1%; Score 998; DB 13; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 CCGTTATCGTCTTGGCTACTGCTGAATGTCCTCCGGAGGAGGAGGAGGCTTTTGC 73
Db 1 CCGTTATCGTCTTGGCTACTGCTGAATGTCCTCCGGAGGAGGAGGAGGCTTTTGC 60
Qy 74 CGTGACCCAGAGATGGCCCGGAGCGAGCAAAATTCCTACTGTCGGCTGCGGGCTACCG 133
Db 61 CGTGACCCAGAGATGGCCCGGAGCGAGCAAAATTCCTACTGTCGGCTGCGGGCTACCG 120
Qy 134 TGGCCCGAGTGAACACTTTCCTCGATCTCAAAAATCGACTCCAAATGCAAGGAG 193
Db 121 TGGCCCGAGTGAACACTTTCCTCGATCTCAAAAATCGACTCCAAATGCAAGGAG 180
Qy 194 AAGCACTCTTGTCTGGTGGAGACGGTGCAGAGAAATCTGCCCTATAGGGGAATGG 253
Db 181 AAGCACTCTTGTCTGGTGGAGACGGTGCAGAGAAATCTGCCCTATAGGGGAATGG 240
Qy 254 TGGCAACGCCCTTAGGATCATTTGAAGAGAGGCTTTCTAAAGCTTTTGGCAAGGATGA 313
```

```
Db 241 TGGCGCACGCCCTTAGGATCATTTGAAGAGGAAGGCTTTCTAAAGAGGAGTGA 300
Qy 314 CACCCGCCATTTACAGACACGCTAGTGTATTCTGAGGTGGAATGGTGCACATATGAACATC 373
Db 301 CACCCGCCATTTACAGACACGCTAGTGTATTCTGAGGTGGAATGGTGCACATATGAACATC 360
Qy 374 TCGAGAGGTTGTGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAATTCAGTCA 433
Db 361 TCGAGAGGTTGTGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAATTCAGTCA 420
Qy 434 TCGAGAGGATGATGGCTGGTGTATTGGCCAGTTTTTACCAATCCAACTGACCTAGTGA 493
Db 421 TCGAGAGGATGATGGCTGGTGTATTGGCCAGTTTTTACCAATCCAACTGACCTAGTGA 480
Qy 494 AGGTTTCAGATGCAAAATGGAAGGAAAAAGAAACTCGAAGGAAAAACATTCGGAATTCGCTG 553
Db 481 AGGTTTCAGATGCAAAATGGAAGGAAAAAGAAACTCGAAGGAAAAACATTCGGAATTCGCTG 540
Qy 554 GTGTACATCATGCTTTTGC AAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCGAG 613
Db 541 GTGTACATCATGCTTTTGC AAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCGAG 600
Qy 614 GCTGGGTACCCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTTAAACCACTTATG 673
Db 601 GCTGGGTACCCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTTAAACCACTTATG 660
Qy 674 ATACAGTGAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCACG 733
Db 661 ATACAGTGAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGACTCACG 720
Qy 734 GTTTATCAAGTTTATGTTCTGGACTGGTACTTCTATTCTGGGAACACACGAGCGGATGCA 793
Db 721 GTTTATCAAGTTTATGTTCTGGACTGGTACTTCTATTCTGGGAACACACGAGCGGATGCA 780
Qy 794 TCAAAAGCAGAAATTAATGAATCAACCAAGAGATAAACAAGGAAGGGGACTTTTGTATAAAT 853
Db 781 TCAAAAGCAGAAATTAATGAATCAACCAAGAGATAAACAAGGAAGGGGACTTTTGTATAAAT 840
Qy 854 CATCGACTGACTGCTTGTATTCTAGGCTGTTCAGGCTGTTCAGGCTGATGAGTCTATATAAAG 913
Db 841 CATCGACTGACTGCTTGTATTCTAGGCTGTTCAGGCTGATGAGTCTATATAAAG 900
Qy 914 GCTTTTACCACCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 973
Db 901 GCTTTTACCACCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG 960
Qy 974 AAAAAATCAGAGAGATGAGTGGAGTCAGTCCATTTTAA 1011
Db 961 AAAAAATCAGAGAGATGAGTGGAGTCAGTCCATTTTAA 998
```

RESULT 15

```
US-10-063-554-125
; Sequence 125, Application US/10063554
; Publication No. US20030040013A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,554
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 125
```

! LENGTH: 998
! TYPE: DNA
! ORGANISM: Homo Sapien
US-10-063-554-125

Query Match 96.1%; Score 998; DB 13; Length 998;
Best Local Similarity 100.0%; Pred. No. 5.3e-312;
Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	14	CCGTTATCGTCTTGGCTACTGCTGAATGTCGCTCCCGAGAGGAGAGGCTTTTGC	73
Db	1	CCGTTATCGTCTTGGCTACTGCTGAATGTCGCTCCCGAGAGGAGAGGCTTTTGC	60
Qy	74	CGCTGACCCAGAGATGGCCGAGCGAGCAAAATCTCTACTCTCGGCTGCGGGCTACCG	133
Db	61	CGCTGACCCAGAGATGGCCGAGCGAGCAAAATCTCTACTCTCGGCTGCGGGCTACCG	120
Qy	134	TGGCCGAGCTAGCAACCTTTCCCTCGGATCTCACAAAACCTCGACTCCAAATGCAAGGAG	193
Db	121	TGGCCGAGCTAGCAACCTTTCCCTCGGATCTCACAAAACCTCGACTCCAAATGCAAGGAG	180
Qy	194	AAGCAGCTCTTCTCGGTTGGGAGACGCTGCAAGAAATCTGCCCTTATAGGGGAATGG	253
Db	181	AAGCAGCTCTTCTCGGTTGGGAGACGCTGCAAGAAATCTGCCCTTATAGGGGAATGG	240
Qy	254	TGCGCACAGCCCTAGGGATCAATGAAGAGGAGCTTTCTAAAGCTTTGGCAAGGAGTGA	313
Db	241	TGCGCACAGCCCTAGGGATCAATGAAGAGGAGCTTTCTAAAGCTTTGGCAAGGAGTGA	300
Qy	314	CACCGCCCATTTACAGACACCTAGTGTATTTCTGAGGTGCAATGGTCAATATGAACATC	373
Db	301	CACCGCCCATTTACAGACACCTAGTGTATTTCTGAGGTGCAATGGTCAATATGAACATC	360
Qy	374	TCCGAGAGTTGCTTTGGCAAAAGTGAAGTGAAGTATCCCTTTTGGAAATCAGTCA	433
Db	361	TCCGAGAGTTGCTTTGGCAAAAGTGAAGTGAAGTATCCCTTTTGGAAATCAGTCA	420
Qy	434	TTGAGGGATGATGGCTGGTGTATTTGGCCAGTTTATTTAGCCAAATCCAACTGACCTAGTGA	493
Db	421	TTGAGGGATGATGGCTGGTGTATTTGGCCAGTTTATTTAGCCAAATCCAACTGACCTAGTGA	480
Qy	494	AGGTTACAGATCAATGGAAGGAAAGGAACTGGAAGGAAACCAATTCGGATTCGTG	553
Db	481	AGGTTACAGATCAATGGAAGGAAAGGAACTGGAAGGAAACCAATTCGGATTCGTG	540
Qy	554	GTGTACATCATGCAATTTGCAAAATCTTAGTGAAGGAGCAATACGAGGCTTTGGGCGAG	613
Db	541	GTGTACATCATGCAATTTGCAAAATCTTAGTGAAGGAGCAATACGAGGCTTTGGGCGAG	600
Qy	614	GCTGGGTACCCCAATATCAAAAGCAGCACTGGTGAATATGGGAGATTTAACCACTTATG	673
Db	601	GCTGGGTACCCCAATATCAAAAGCAGCACTGGTGAATATGGGAGATTTAACCACTTATG	660
Qy	674	ATACAGTGAACACTACTGCTGTAATGCAATACCACTTGAAGGAGCAATATCATGACTCAG	733
Db	661	ATACAGTGAACACTACTGCTGTAATGCAATACCACTTGAAGGAGCAATATCATGACTCAG	720
Qy	734	GTTTATCAAGTTTATGTTCTGGACTGGTACTGTTCTATTTCTGGGAAACACAGCCGATGCA	793
Db	721	GTTTATCAAGTTTATGTTCTGGACTGGTACTGTTCTATTTCTGGGAAACACAGCCGATGCA	780
Qy	794	TCAAAGCAGAAATGAATCAACAGGAGATAAACAAGGAGGGGACTTTTGTATATAAT	853
Db	781	TCAAAGCAGAAATGAATCAACAGGAGATAAACAAGGAGGGGACTTTTGTATATAAT	840
Qy	854	CATCGACTGACTGCTGATTGATTCAGGCTGTTCAAGGTGAAGATTTCATGACTTATATAAG	913
Db	841	CATCGACTGACTGCTGATTGATTCAGGCTGTTCAAGGTGAAGATTTCATGACTTATATAAG	900
Qy	914	GCTTTTATCAATCTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG	973
Db	901	GCTTTTATCAATCTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTTGGCTTACTTATG	960

Qy	974	AAAAATCAGAGAGATGAGTGGAGTCAGTCCATTTAA	1011
Db	961	AAAAATCAGAGAGATGAGTGGAGTCAGTCCATTTAA	998

Search completed: September 24, 2004, 09:23:23
Job time : 3503 secs